

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 10, 2001, 08:36:07 ; Search time 33.27 Seconds
(without alignments)
35.790 Million cell updates/sec

Title: US-09-489-760-5
Perfect score: 42
Sequence: 1 VLRLDLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL16.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_plant.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_unclassified.*
- 13: sp_vertebrate.*
- 14: sp_virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	1165	4	Q92619
2	38	90.5	4150	2	Q9KIV3
3	36	85.7	174	5	Q94256
4	35	83.3	616	1	O27025
5	34	81.0	238	14	Q9WHX7
6	34	81.0	239	14	Q9WHY9
7	34	81.0	239	14	Q9WHY8
8	34	81.0	239	14	Q9WHY7
9	34	81.0	239	14	Q9WHY6
10	34	81.0	239	14	Q9WHY5
11	34	81.0	239	14	Q9WHY4
12	34	81.0	239	14	Q9WHY3
13	34	81.0	239	14	Q9WHY1
14	34	81.0	239	14	Q9WHX9
15	34	81.0	250	14	Q9WHY2
16	34	81.0	252	14	Q93188
17	34	81.0	389	2	Q9XTD7
18	34	81.0	486	2	Q9PPU0
19	34	81.0	791	5	Q9NG78

20	34	81.0	3816	2	Q9KIV3
21	33	78.6	300	2	Q9KFG3
22	33	78.6	324	10	P93619
23	33	78.6	377	8	O09424
24	33	78.6	392	8	Q36681
25	33	78.6	396	8	O09418
26	33	78.6	396	8	O09426
27	33	78.6	432	8	O78605
28	33	78.6	435	8	O09416
29	33	78.6	437	8	O09422
30	33	78.6	440	8	Q33148
31	33	78.6	441	8	Q31822
32	33	78.6	465	8	Q31907
33	33	78.6	465	8	Q32207
34	33	78.6	465	8	Q32484
35	33	78.6	465	8	Q33136
36	33	78.6	465	8	Q33509
37	33	78.6	466	8	O20245
38	33	78.6	467	8	O9TLN7
39	33	78.6	469	8	Q9GDP7
40	33	78.6	475	8	Q9MTF0
41	33	78.6	833	10	Q9LV01
42	32	76.2	237	2	O06978
43	32	76.2	274	5	Q9W157
44	32	76.2	389	2	O86581
45	32	76.2	452	3	O43088

ALIGNMENTS

RESULT 1

Q92619 ID Q92619 PRELIMINARY; PRT: 1165 AA.
AC Q92619;
DT 01-FEB-1997 (TEMBLrel. 02, Created)
DT 01-FEB-1997 (TEMBLrel. 02, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE MYELOBLAST KIAA0223 (FRAGMENT).
GN KIAA0223.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.

RX TISSUE-BONE MARROW;

RC MEDLINE-97191544; PubMed-9039502; Ohira M., Kawarabayasi Y., Ohara O.,

RA Nagase T., Seki N., Ishikawa K., Miyajima N., Nomura N.;

RA Tanaka A., Kotani H., Miyajima N., Nomura N.;

RA "Prediction of the coding sequences of unidentified human genes. VI.

RT The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by

RT analysis of cDNA clones from cell line KG-1 and brain."

RL DNA Res. 3:321-329(1996).

RN [2]

RP SEQUENCE OF 170-1165 FROM N.A.

RX Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,

RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,

RA Phan H., Velasco N., Garnes J., Danganan L., Poundstone P.,

RA Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T.,

RA Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,

RA Bruce R., Thomas P., Quan G., Krommiller B., Arellano A.,

RA Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,

RA Carrano A.V.;

RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; D86976; BAA13212.1; -

DR EMBL; AC004151; AAC03237.1; -

DR HSSP; Q07960; IRGP.

DR InterPro; IPR000198; -

DR InterPro; IPR002219; -

DR Pfam; PF001130; DAG_PE-bind; 1.

DR Pfam; PF00620; RHOGAP; 1.

DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; UNKNOWN_1.

DR PROSITE; PS0081; DAG_PE_BIND_DOM_2; 1.
 DR SMART; SM00324; RhogAP; 1.
 FT NON_TER 1
 SQ SEQUENCE 1165 AA; 127344 MW; 92EF768CAED458C9 CRC64;

Query Match 100.0%; Score 42; DB 4; Length 1165;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLKDDLEA 9
 |||||
 Db 166 VLKDDLEA 174

RESULT 2
 ID Q9KIV4 PRELIMINARY; PRT; 4150 AA.

AC Q9KIV4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE 8, 8A-DEOXYOLEANOLIDE SYNTHASE 1.
 GN OLEA1.
 OS Streptomyces antibioticus.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1890;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20363406; PubMed=10908114;
 RA Shah S., Xue Q., Tang L., Carney J.R., Betlach M., McDaniel R.;
 RT "Cloning, Characterization, and Heterologous Expression of a
 RT Polyketide Synthase and P-450 Oxidase Involved in the Biosynthesis of
 RT the Antibiotic Oleandomycin";
 RL J. Antibiot. 53:502-508(2000).
 DR EMBL; AF220951; AAF82408.1; -.
 DR InterPro; IPR000169; -.
 DR InterPro; IPR000255; -.
 DR InterPro; IPR000794; -.
 DR InterPro; IPR001227; -.
 DR InterPro; IPR002106; -.
 DR Pfam; PF00109; ketoacyl-synt; 3.
 DR Pfam; PF00550; pp-binding; 3.
 DR Pfam; PF00698; Acyl_transf; 3.
 DR PROSITE; PS00339; AA_TRNA_LIGASE_IL_2; UNKNOWN_1.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 2.
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 3.
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
 KW Phosphopantetheine; Transferase.
 SQ SEQUENCE 4150 AA; 435266 MW; 9383296C4C16647D CRC64;

Query Match 90.5%; Score 38; DB 2; Length 4150;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LRDDLEA 9
 |||||
 Db 1781 LRDDLEA 1788

RESULT 3
 ID Q94256 PRELIMINARY; PRT; 174 AA.

AC Q94256;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE COSMID K04A8.
 GN K04A8.9;
 OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
 RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX Geisel C., Bradshaw H.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U64849; AAC48055.1; -.
 DR InterPro; IPR000004; -.
 DR SMART; SM00118; SAPB; 1.
 SQ SEQUENCE 174 AA; 19210 MW; A6303CF6383BED9 CRC64;

Query Match 85.7%; Score 36; DB 5; Length 174;
 Best Local Similarity 77.8%; Pred. No. 23;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLKDDLEA 9
 ||:||||:
 Db 129 VLKDDLEA 137

RESULT 4

ID 027025 PRELIMINARY; PRT; 616 AA.
 AC 027025;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE TYPE I RESTRICTION MODIFICATION ENZYME, SUBUNIT M.
 GN MTH942.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
 OC Methanothermobacter.
 OX NCBI_TaxID=145262;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DELTA H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., DuBois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
 RA Spadaro R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 RT deltaH: functional analysis and comparative genomics.";
 RL J. Bacteriol. 179:7135-7155(1997).
 DR EMBL; AE000868; AB85440.1; -.
 DR InterPro; IPR002052; -.
 DR InterPro; IPR002296; -.
 DR InterPro; IPR003356; -.
 DR Pfam; PF02384; N6_Mtase; 1.
 DR PRINTS; PR00507; N12NGMTFRASE.

DR PROSITE: PS00092; NG_MTASE: UNKNOWN.1.
SQ SEQUENCE 616 AA; 71715 MW; 06DAF1076A5D5BAD CRC64;

Query Match 83.3%; Score 35; DB 1; Length 616;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLRDDLLLEA 9
||| ||| |||
Db 465 VLEDDLLIEA 473

RESULT 5

ID Q9WHX7 PRELIMINARY; PRT; 238 AA.
AC Q9WHX7;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE MATRIX PROTEIN M1 (FRAGMENT).
GN M.
OS Influenza A virus (A/Taiwan/96/179).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
OX NCBI_TaxID-94648;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/TAIWAN/96/179;
RA Shih S.-R., Tsai H.-R., Chang S.-C.;
RT "Sequence Analysis of M Gene of Influenza A Viruses Isolated in Taiwan";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF138707; AAD33736.2; -.
DR HSSP; P03485; 1AA7.
DR InterPro; IPR001561; -.
DR Pfam; PF00598; Flu_M1; 1.
DR ProDom; PD001061; -; 1.
KW Matrix protein.
FT NON_TER 1
SQ SEQUENCE 238 AA; 26266 MW; 401A494B5B673FOA CRC64;

Query Match 81.0%; Score 34; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LRDDLLLE 8
|||||||
Db 215 LRDDLLLE 221

RESULT 6

ID Q9WHY9 PRELIMINARY; PRT; 239 AA.
AC Q9WHY9;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE MATRIX PROTEIN M1 (FRAGMENT).
GN M.
OS Influenza A virus (A/Taiwan/98/346).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
OX NCBI_TaxID-94660;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/TAIWAN/98/346;
RA Shih S.-R., Tsai H.-R., Chang S.-C.;
RT "Sequence Analysis of M Gene of Influenza A Viruses Isolated in Taiwan";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF138719; AAD33768.2; -.

DR HSSP; P03485; 1AA7.
DR InterPro; IPR001561; -.
DR Pfam; PF00598; Flu_M1; 1.
KW Matrix protein.
FT NON_TER 1
SQ SEQUENCE 239 AA; 26462 MW; 2BD3359212691DD8 CRC64;

Query Match 81.0%; Score 34; DB 14; Length 239;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LRDDLLLE 8
|||||||
Db 216 LRDDLLLE 222

RESULT 7

ID Q9WHY8 PRELIMINARY; PRT; 239 AA.
AC Q9WHY8;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE MATRIX PROTEIN M1 (FRAGMENT).
GN M.
OS Influenza A virus (A/Taiwan/98/224).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
OX NCBI_TaxID-94659;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/TAIWAN/98/224;
RA Shih S.-R., Tsai H.-R., Chang S.-C.;
RT "Sequence Analysis of M Gene of Influenza A Viruses Isolated in Taiwan";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF138718; AAD33767.2; -.
DR HSSP; P03485; 1AA7.
DR InterPro; IPR001561; -.
DR Pfam; PF00598; Flu_M1; 1.
DR ProDom; PD001061; -; 1.
KW Matrix protein.
FT NON_TER 1
SQ SEQUENCE 239 AA; 26411 MW; 2935533A39097E3E4 CRC64;

Query Match 81.0%; Score 34; DB 14; Length 239;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LRDDLLLE 8
|||||||
Db 216 LRDDLLLE 222

RESULT 8

ID Q9WHY7 PRELIMINARY; PRT; 239 AA.
AC Q9WHY7;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE MATRIX PROTEIN M1 (FRAGMENT).
GN M.
OS Influenza A virus (A/Taiwan/98/45).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
OX NCBI_TaxID-94658;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/TAIWAN/98/45;
RA Shih S.-R., Tsai H.-R., Chang S.-C.;

RT "Sequence Analysis of M Gene of Influenza A Viruses Isolated in
 RL Taiwan."
 RC Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF138717; AAD33766.2; -.
 DR HSSP; P03485; IAA7.
 DR InterPro; IPR001561; -.
 DR Pfam; PF00598; Flu_M1; 1.
 DR ProDom; PD001061; -; 1.
 KW Matrix protein.
 FT NON_TER 1
 SQ SEQUENCE 239 AA; 26381 MW; B24B9F220299ECD9 CRC64;

Query Match 81.0%; Score 34; DB 14; Length 239;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLLE 8
 Db 216 LRDDLLE 222

RESULT 9
 Q9WHY6 PRELIMINARY; PRT; 239 AA.
 AC Q9WHY6;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE MATRIX PROTEIN M1 (FRAGMENT).
 GN M.
 OS Influenza A virus (A/Taiwan/98/21).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
 OX NCBI_TaxID=94657;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A/TAIWAN/98/21;
 RA Shih S.-R., Tsai H.-R., Chang S.-C.;
 RT "Sequence Analysis of M Gene of Influenza A Viruses Isolated in
 Taiwan."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF138716; AAD33765.2; -.
 DR HSSP; P03485; IAA7.
 DR InterPro; IPR001561; -.
 DR Pfam; PF00598; Flu_M1; 1.
 DR ProDom; PD001061; -; 1.
 KW Matrix protein.
 FT NON_TER 1
 SQ SEQUENCE 239 AA; 26298 MW; 6F9A44A4FBFC74BD CRC64;

Query Match 81.0%; Score 34; DB 14; Length 239;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLLE 8
 Db 216 LRDDLLE 222

RESULT 10
 Q9WHY5 PRELIMINARY; PRT; 239 AA.
 AC Q9WHY5;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE MATRIX PROTEIN M1 (FRAGMENT).
 GN M.
 OS Influenza A virus (A/Taiwan/98/20).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.

OX NCBI_TaxID=94656;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A/TAIWAN/98/20;
 RA Shih S.-R., Tsai H.-R., Chang S.-C.;
 RT "Sequence Analysis of M Gene of Influenza A Viruses Isolated in
 Taiwan."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF138715; AAD33764.2; -.
 DR HSSP; P03485; IAA7.
 DR InterPro; IPR001561; -.
 DR Pfam; PF00598; Flu_M1; 1.
 DR ProDom; PD001061; -; 1.
 KW Matrix protein.
 FT NON_TER 1
 SQ SEQUENCE 239 AA; 26275 MW; 6C345804B4B2C7AC CRC64;

Query Match 81.0%; Score 34; DB 14; Length 239;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLLE 8
 Db 216 LRDDLLE 222

RESULT 11
 Q9WHY4 PRELIMINARY; PRT; 239 AA.
 AC Q9WHY4;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE MATRIX PROTEIN M1 (FRAGMENT).
 GN M.
 OS Influenza A virus (A/Taiwan/97/3469).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
 OX NCBI_TaxID=94655;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A/TAIWAN/97/3469;
 RA Shih S.-R., Tsai H.-R., Chang S.-C.;
 RT "Sequence Analysis of M Gene of Influenza A Viruses Isolated in
 Taiwan."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF138714; AAD33763.2; -.
 DR HSSP; P03485; IAA7.
 DR InterPro; IPR001561; -.
 DR Pfam; PF00598; Flu_M1; 1.
 DR ProDom; PD001061; -; 1.
 KW Matrix protein.
 FT NON_TER 1
 SQ SEQUENCE 239 AA; 26397 MW; 6E215E154BFC64AC CRC64;

Query Match 81.0%; Score 34; DB 14; Length 239;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLLE 8
 Db 216 LRDDLLE 222

RESULT 12
 Q9WHY3 PRELIMINARY; PRT; 239 AA.
 AC Q9WHY3;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE MATRIX PROTEIN M1 (FRAGMENT).
GN M.
OS Influenza A virus (A/Taiwan/97/3351).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
OX NCBI_TaxID=94654;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/TAIWAN/97/3351;
RA Shih S.-R., Tsai H.-R., Chang S.-C.;
RT "Sequence Analysis of M Gene of Influenza A Viruses Isolated in Taiwan."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF138713; AAD33762.2; -.
DR HSSP; P03485; IAA7.
DR InterPro; IPR001561; -.
DR Pfam; PF00598; Flu_M1; 1.
DR ProDom; PD001061; -. 1.
KW Matrix protein.
FT NON_TER 1
SQ SEQUENCE 239 AA; 26284 MW; 598A982BB966975A CRC64;

Query Match 81.0%; Score 34; DB 14; Length 239;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLLE 8
Db 216 LRDDLLE 222

RESULT 13
Q9WHY1 ID Q9WHY1 PRELIMINARY; PRT; 239 AA.
AC Q9WHY1;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE MATRIX PROTEIN M1 (FRAGMENT).
GN M.
OS Influenza A virus (A/Taiwan/96/2191).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
OX NCBI_TaxID=94652;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/TAIWAN/96/2191;
RA Shih S.-R., Tsai H.-R., Chang S.-C.;
RT "Sequence Analysis of M Gene of Influenza A Viruses Isolated in Taiwan."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF138711; AAD33760.2; -.
DR HSSP; P03485; IAA7.
DR InterPro; IPR001561; -.
DR Pfam; PF00598; Flu_M1; 1.
DR ProDom; PD001061; -. 1.
KW Matrix protein.
FT NON_TER 1
SQ SEQUENCE 239 AA; 26439 MW; 8151D148E9968759 CRC64;

Query Match 81.0%; Score 34; DB 14; Length 239;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLLE 8
Db 216 LRDDLLE 222

RESULT 14
Q9WHX9

ID Q9WHX9 PRELIMINARY; PRT; 239 AA.
Q9WHX9;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE MATRIX PROTEIN M1 (FRAGMENT).
GN M.
OS Influenza A virus (A/Taiwan/96/1600).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
OX NCBI_TaxID=94650;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/TAIWAN/96/1600;
RA Shih S.-R., Tsai H.-R., Chang S.-C.;
RT "Sequence Analysis of M Gene of Influenza A Viruses Isolated in Taiwan."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF138709; AAD33758.2; -.
DR HSSP; P03485; IAA7.
DR InterPro; IPR001561; -.
DR Pfam; PF00598; Flu_M1; 1.
DR ProDom; PD001061; -. 1.
KW Matrix protein.
FT NON_TER 1
SQ SEQUENCE 239 AA; 26407 MW; F8CAB96A8644455E CRC64;

Query Match 81.0%; Score 34; DB 14; Length 239;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLLE 8
Db 216 LRDDLLE 222

RESULT 15
Q9WHY2 ID Q9WHY2 PRELIMINARY; PRT; 250 AA.
AC Q9WHY2;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE MATRIX PROTEIN M1 (FRAGMENT).
GN M.
OS Influenza A virus (A/Taiwan/96/3513).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
OX NCBI_TaxID=94653;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/TAIWAN/96/3513;
RA Shih S.-R., Tsai H.-R., Chang S.-C.;
RT "Sequence Analysis of M Gene of Influenza A Viruses Isolated in Taiwan."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF138712; AAD33761.1; -.
DR HSSP; P03485; IAA7.
DR InterPro; IPR001561; -.
DR Pfam; PF00598; Flu_M1; 1.
DR ProDom; PD001061; -. 1.
KW Matrix protein.
FT NON_TER 1
SQ SEQUENCE 250 AA; 27671 MW; A47536EC384C3FBC CRC64;

Query Match 81.0%; Score 34; DB 14; Length 250;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLLE 8
Db 216 LRDDLLE 222

Tue Jul 10 13:30:21 2001

us-09-489-760-5.rspt

Page 6

Db 227 LRDDLE 233

Search completed: July 10, 2001, 08:36:07
Job time: 260 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 10, 2001, 08:28:11 ; Search time 22.85 Seconds
(without alignments)
30.003 Million cell updates/sec

Title: US-09-489-760-2

Perfect score: 45

Sequence: 1 VLHDDLEA 9

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	84.4	1148	2 S51855	hypothetical prote
2	35	77.8	119	2 T00151	hypothetical prote
3	35	77.8	604	2 S36487	El protein - human
4	35	77.8	605	2 S36469	El protein - human
5	35	77.8	616	2 C69226	type I restriction
6	34	75.6	130	2 A81316	chemotaxis regulat
7	33	73.3	145	2 A41652	probable glyceroph
8	33	73.3	210	2 T44122	probable glyceroph
9	33	73.3	238	2 S76860	hypothetical prote
10	33	73.3	259	2 G82601	conserved hypothet
11	33	73.3	291	2 D83371	probable dehydroge
12	33	73.3	320	2 B75457	polyprenyl synthas
13	33	73.3	322	2 C83075	octaprenyl-dihosph
14	33	73.3	343	2 A45251	DNA directed DNA p
15	33	73.3	343	2 B95564	DNA polymerase III
16	33	73.3	378	2 T36403	probable polypreny
17	33	73.3	397	2 S09813	hypothetical prote
18	33	73.3	398	2 H72660	probable N-Acylami
19	33	73.3	519	1 S69988	unspecific monooxy
20	33	73.3	519	1 S69989	unspecific monooxy
21	33	73.3	604	2 S36493	El protein - human
22	33	73.3	667	2 H85734	probable collagena
23	33	73.3	667	2 F64895	hypothetical prote
24	33	73.3	723	2 F85047	hypothetical prote
25	33	73.3	856	2 C85023	secA protein [limp
26	33	73.3	908	2 T50695	hypothetical prote
27	33	73.3	973	2 T50449	DNA repair and rec
28	33	73.3	1127	2 T47445	MDM1 protein - yea
29	33	73.3	1770	2 S56221	hypothetical prote

ALIGNMENTS

RESULT 1

S51855
hypothetical protein YDR128w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YD9302.03

C:Species: Saccharomyces cerevisiae

C>Date: 05-May-1995 #sequence_revision 21-Jul-1995 #text_change 26-May-2000

C:Accession: S51855

R:Oliver, K.; Harris, D.

submitted to the EMBL Data Library, February 1995

A:Reference number: S51853

A:Accession: S51855

A:Molecule type: DNA

A:Residues: 1-1148 <OLI>

A:Cross-references: EMBL:Z48179; NID:9665657; PID:9665660; GSPDB:GM000004; MIPS:YDR128

C:Genetics:

A:Gene: MIPS:YDR128w

A:Map position: 4R

C:Superfamily: unassigned WD repeat proteins; WD repeat homology

Query Match 84.4%; Score 38; DB 2; Length 1148;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHDDLEA 9
:||||:|
DB 1001 LLHDDIEA 1009

RESULT 2

T00151
hypothetical protein 18 - Staphylococcus aureus phage phi PVL

C:Species: Staphylococcus aureus phage phi PVL

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jul-2000

C:Accession: T00151

R:Kaneko, J.; Kimura, T.; Tomita, T.; Kamio, Y.

Biosci. Biotechnol. Biochem. 61, 1960-1962, 1997

A:Title: Pantone-Valentine leukocidin genes in a phage-like particle isolated from ml

A:Reference number: Z14119; MUID:98067870

A:Accession: T00151

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-119 <KAN>

A:Cross-references: EMBL:AB009866; NID:g3341907; PIDN:BAA31891.1; PID:g3341925

C:Superfamily: Staphylococcus aureus phage phi PVL hypothetical protein 18

Query Match

Best Local Similarity 77.8%; Score 35; DB 2; Length 119;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDDLLEA 9

Db 72 HDDILEA 78
|||||

RESULT 3

S36487
EI protein - human papillomavirus type 19

C:Species: human papillomavirus type 19
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C:Accession: S36487

R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36487

A:Molecule type: DNA

A:Residues: 1-604

A:Cross-references: EMBL:X74470; NID:g396940; PIDN:CAA52520.1; PID:g396943

C:Superfamily: papillomavirus EI protein

C:Keywords: early protein; nucleus

Query Match

Best Local Similarity 77.8%; Score 35; DB 2; Length 604;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHDDLEA 9

|||||

Db 201 VHDDLES 208

RESULT 4

S36469
EI protein - human papillomavirus type 14D

C:Species: human papillomavirus type 14D
C>Date: 09-Dec-1993 #sequence_revision 26-Jul-1996 #text_change 26-Aug-1999

C:Accession: S36469

R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36469

A:Molecule type: DNA

A:Residues: 1-605

A:Cross-references: EMBL:X74467; NID:g396918; PIDN:CAA52502.1; PID:g396919

A:Experimental source: strain 14D

C:Superfamily: papillomavirus EI protein

C:Keywords: early protein; nucleus

Query Match

Best Local Similarity 77.8%; Score 35; DB 2; Length 605;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHDDLEA 9

|||||

Db 202 VHDDLES 209

RESULT 5

C69226

type I restriction modification enzyme, subunit M - Methanobacterium thermoautotrophicum

C:Species: Methanobacterium thermoautotrophicum

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999

C:Accession: C69226

R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

Qu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;

ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct

A:Reference number: A69000; MUID:98037514

A:Accession: C69226

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-616 <MTH>

A:Cross-references: GB:AE000868; GB:AE000666; NID:g2622025; PIDN:AAB85440.1; PID:g2622025

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH942

A:Start codon: GTG

C:Superfamily: type I site-specific deoxyribonuclease chain hsdM

Query Match

Best Local Similarity 77.8%; Score 35; DB 2; Length 616;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLEA 9

|||||

Db 465 VLEDDLEA 473

RESULT 6

A81316

chemotaxis regulatory protein Cj1118c [Imported] - Campylobacter jejuni (strain NCTC

C:Species: Campylobacter jejuni

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000

C:Accession: A81316

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chil

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Ba

Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals

A:Reference number: A81250; MUID:20150912

A:Accession: A81316

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-130 <PAB>

A:Cross-references: GB:A1139077; GB:A1111168; NID:g6968444; PIDN:CAB73373.1; PID:g696

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:

A:Gene: cheY; Cj1118c

C:Superfamily: chemotaxis cheY protein; response regulator homology

Query Match

Best Local Similarity 75.6%; Score 34; DB 2; Length 130;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDLLEA 9

|||||

Db 25 HDVLEA 31

RESULT 7

A41652

probable glycerophosphodiester phosphodiesterase (EC 3.1.4.46) - Staphylococcus aureus

C:Species: Staphylococcus aureus

C>Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 15-Oct-1999

C:Accession: A41652

R:Ryffel, C.; Bucher, R.; Kayser, F.H.; Berger-Baechi, B.

J. Bacteriol. 173, 7416-7422, 1991

A:Title: The Staphylococcus aureus mec determinant comprises an unusual cluster of di

terase.

A:Reference number: A41652; MUID:92041650

A:Accession: A41652

A:Molecule type: DNA

A:Residues: 1-145 <RYF>

A:Cross-references: GB:X52594; NID:g48712; PIDN:CAA36830.1; PID:g48713

C:Keywords: phosphoric diester hydrolase

Query Match

Best Local Similarity 73.3%; Score 33; DB 2; Length 145;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLE 8

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 10, 2001, 08:31:41 ; Search time 22.85 Seconds
(without alignments)
30.003 Million cell updates/sec

Title: DS-09-489-760-5
Perfect score: 42
Sequence: 1 VLRDDLLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

```

```
Database :      PIR_68:*
1:  pir1:*
2:  pir2:*
3:  pir3:*
4:  pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length	%			
1	35	83.3	616	2	C69226	type I restriction	
2	34	81.0	282	2	S31258	probable membrane	
3	34	81.0	343	2	A64443	glyceroldehyde-3-p	
4	34	81.0	389	2	T20604	hypothetical prote	
5	34	81.0	486	2	A82878	replicative DNA he	
6	34	81.0	3519	2	SA3048	polyketide synthas	
7	33	78.6	300	2	DB3714	surface adhesin A	
8	33	78.6	324	2	T11672	quinone oxidoreduc	
9	33	78.6	483	2	H85073	probable transposo	
10	33	78.6	822	2	I38728	epidermal growth f	
11	33	78.6	1041	2	E70760	probable iles prot	
12	32	76.2	237	2	D70032	two-component resp	
13	32	76.2	264	2	T41578	hypothetical prote	
14	32	76.2	335	2	A64988	hypothetical 37.8	
15	32	76.2	335	2	H85857	hypothetical prote	
16	32	76.2	372	2	D70753	probable oxidoredu	
17	32	76.2	389	2	T34766	iron-sulfur cofact	
18	32	76.2	452	2	T40769	hypothetical prote	
19	32	76.2	499	2	G86538	leucyl aminopeptid	
20	32	76.2	499	2	G72083	leucine aminopepti	
21	32	76.2	545	2	T00485	probable phosphori	
22	32	76.2	568	2	DB3182	hypothetical prote	
23	32	76.2	587	2	E71020	hypothetical prote	
24	32	76.2	599	1	A42331	sulfite reductase	
25	32	76.2	599	1	H85057	sulfite reductase	
26	32	76.2	599	2	DB5926	hypothetical prote	
27	32	76.2	826	2	T46060	hypothetical prote	
28	32	76.2	826	2	T46061	hypothetical prote	
29	32	76.2	889	2	T02240	nitrate reductase	

ALIGNMENTS

RESULT

RESOL
C69226

cos2250
 restriction modification enzyme, subunit M - Methanobacterium thermoautotrophilum
 Species: Methanobacterium thermoautotrophicum
 C:Species: Methanobacterium thermoautotrophicum
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
 C:Accession: C59226
 C:Accession: C59226
 C:Author: Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.
 C:Title: Qiu, D.; Spadafora, R.; Vacaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 C:Journal: J. Bacteriol. 179, 7135-7155, 1997
 C:Abstract: A complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu
 A:Accession: C59226
 A:Reference number: A59000; MUID:98037514
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-616 <MTH>
 A:Cross-references: GB:AE000868; GB:AE000566; NID:g2622025; PIDN:AAB85440.1; PID:g262
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MTH942
 A:Start codon: GTG
 A:Superfamily: type I site-specific deoxyribonuclease chain bsdm

Query Match 83.3%; Score 35; DB 2; Length 616;
Best Local Similarity 77.8%; Pred. No. 46;
Matches 7. Conservative 1. Mismatches 1. Indels 0. Gaps 0.

QY 1 VLRDDLLEA 9
465 VLEDDLEA 473

REPORT

05017050
RESULT

S31258
probable membrane protein FUN34 - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: protein N209; protein YNR002C
C:Species: *Saccharomyces cerevisiae*
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
C:Accession: S31258; S45126; S48340; S63328
C:Author: R. R. Stettler, S. Mariotte, S. Riva, M.; Sentenac, A.; Thuriaux, P.
J. Biol. Chem. 267, 21390-21395, 1992
A:Title: An essential and specific subunit of RNA polymerase III (C) is encoded by 9,
A:Reference number: A45107; MUID:93016077
A:Accession: S31258
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-282 <STE>
A:Cross-references: EMBL:X63746; NID:q4378; PIDN:CA945279.1; PID:q4380
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 199
R:Rivhasselt, P.; Aert, R.; Voet, M.; Volckaert, G.
submitted to the EMBL Data Library, January 1994

A:Description: Twelve open reading frames revealed on the 23.6 kbp segment flanking the
 A:Reference number: S45119
 A:Accession: S45126
 A:Molecule type: DNA
 A:Residues: 1-282 <VER>
 A:Cross-references: EMBL:X77395; NID:g496717; PIDN:CAA54571.1; PID:g496720
 R:Verhasselt, P.; Aert, R.; Voet, M.; Volckaert, G.
 Yeast 10, 1355-1361, 1994
 A:Title: Twelve open reading frames revealed in the 23.6 kb segment flanking the centromere
 A:Reference number: S48338; MUID:95208356
 A:Accession: S48340
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-282 <VE2>
 A:Cross-references: EMBL:X77395; NID:g496717; PIDN:CAA54571.1; PID:g496720
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1994
 R:Aert, R.; Verhasselt, P.; Voet, M.; Volckaert, G.
 submitted to the Protein Sequence Database, April 1996
 A:Reference number: S62910
 A:Accession: S63328
 A:Molecule type: DNA
 A:Residues: 1-282 <AER>
 A:Cross-references: EMBL:X77395; NID:g1302470; PIDN:CAA96278.1; PID:g1302471; MIPS:YNR00C
 A:Experimental source: strain 5288C
 C:Genetics:
 A:Gene: SGD:FUN34
 A:Cross-references: SGD:S0005285; MIPS:YNR002c
 A:Map position: 14R
 C:Superfamily: Saccharomyces cerevisiae probable membrane protein FUN34
 C:Keywords: transmembrane protein
 F:119-135/Domain: transmembrane #status predicted <TM1>
 F:186-202/Domain: transmembrane #status predicted <TM2>
 F:209-225/Domain: transmembrane #status predicted <TM3>
 F:234-250/Domain: transmembrane #status predicted <TM4>

Query Match 81.0%; Score 34; DB 2; Length 282;
 Best Local Similarity 87.5%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 LRDDLLEA 9
 |||||
 DB 62 LRDDLFEA 69

RESULT 3
 A6443
 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C:Accession: A6443
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Rondon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A:Reference number: A64300; MUID:9637999
 A:Accession: A6443
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-343 <BU1>
 A:Cross-references: GB:U67557; GB:L77117; NID:g1591777; PIDN:AAB99147.1; PID:g1591778; MIPS:YNR00C
 C:Genetics:
 A:Map position: REV1086336-1085305
 C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase
 C:Keywords: oxidoreductase

Query Match 81.0%; Score 34; DB 2; Length 343;
 Best Local Similarity 77.8%; Pred. No. 38;
 Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 VLRDDLLEA 9
 |||||
 DB 238 VSRDDLLEA 246

RESULT 4

T20604
 hypothetical protein Y51H1A.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T20604; T27102
 R:Wallis, J.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19298
 A:Accession: T20604
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-389 <WIL>
 A:Cross-references: EMBL:Z81495; PIDN:CA804064.1; GSPDB:GN00020; CESP:Y51H1A.1
 A:Experimental source: clone F08G2
 R:Smyle, R.
 submitted to the EMBL Data Library, October 1998
 A:Reference number: Z20309
 A:Accession: T27102
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-389 <W12>
 A:Cross-references: EMBL:AL032644; PIDN:CAA21673.1; GSPDB:GN00020; CESP:Y51H1A.1
 A:Experimental source: clone Y51H1A
 C:Genetics:
 A:Gene: CESP:Y51H1A.1
 A:Map position: 2
 A:Introns: 12/3; 38/3; 167/2; 276/1; 342/3

Query Match 81.0%; Score 34; DB 2; Length 389;
 Best Local Similarity 87.5%; Pred. No. 44;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLLEA 9
 |||||
 DB 21 LRDELLEA 28

RESULT 5

A82878
 replicative DNA helicase U0550 [imported] - Ureaplasma urealyticum
 C:Species: Ureaplasma urealyticum
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C:Accession: A82878
 R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
 submitted to GenBank, February 2000
 A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a
 A:Reference number: A82870
 A:Accession: A82878
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-486 <GLA>
 A:Cross-references: GB:AF002153; GB:AF222894; NID:g6899544; PIDN:AAF30963.1; GSPDB:GN
 A:Experimental source: serovar 3; biovar 1
 C:Genetics:
 A:Gene: dnab; U0550
 A:Genetic code: SGC3

Query Match 81.0%; Score 34; DB 2; Length 486;
 Best Local Similarity 75.0%; Pred. No. 56;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLLEA 9
 :|||||
 DB 445 MRDDLLEA 452

A:Title: Evolutionary conservation of the EPS8 gene and its mapping to human chromosome
 A:Reference number: I38728; MUID:94366758
 A:Accession: I38728
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-822 <RES>
 A:Cross-references: EMBL:U12535; NID:g530822; PID:g530823
 C:Genetics:
 A:Gene: Eps8
 C:Superfamily: SH3 homology

Query Match 78.6%; Score 33; DB 2; Length 822;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLKDDLE 8
 |||||
 Db 552 VLKDDLE 559

RESULT 11

E70760
 probable ilcs protein - Mycobacterium tuberculosis (strain H37Rv)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
 C:Accession: E70760
 R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987
 A:Accession: E70760
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1041 <COL>
 A:Cross-references: GB:Z74020; GB:AL123456; NID:g3261584; PIDN:CAA98326.1; PID:g1403506
 A:Experimental source: strain H37Rv
 C:Genetics:
 A:Gene: ilcs
 C:Superfamily: isoleucine--trna ligase

Query Match 78.6%; Score 33; DB 2; Length 1041;
 Best Local Similarity 77.8%; Pred. No. 2e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLKDDLEA 9
 |||||
 Db 710 VLKDDLEA 718

RESULT 12

D70032
 two-component response regulator [YvcQ] homolog yvcP - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
 C:Accession: D70032
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
 C.; Bron, S.; Brouillet, S.; Bruschini, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, P.M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, M

A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
 A:Reference number: A69580; MUID:98044033
 A:Accession: D70032
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-237 <KUN>
 A:Cross-references: GB:Z99121; GB:AL009136; NID:g2635827; PIDN:CAB15477.1; PID:g26359
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yvcP
 C:Superfamily: ompR protein; response regulator homology
 C:Keywords: phosphoprotein
 F:4-112/Domain: response regulator homology <RRH>
 F:52/Binding site: phosphate (Asp) (covalent) #status predicted

Query Match 76.2%; Score 32; DB 2; Length 237;
 Best Local Similarity 77.8%; Pred. No. 63;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLKDDLEA 9
 |||||
 Db 176 VSRDELLEA 184

RESULT 13

T41578
 hypothetical protein SPC737.05 - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Feb-2000
 C:Accession: T41578
 R:Murphy, L.; Harris, D.; Wood, V.; Lyne, M.H.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, September 1998
 A:Reference number: Z22002
 A:Accession: T41578
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-264 <MUR>
 A:Cross-references: EMBL:AL031546; NID:el375214; PIDN:CAB44773.1; GSPDB:GN00068; SPDB
 A:Experimental source: strain 972h(-)
 C:Genetics:
 A:Gene: SPDB:SPCC737.05
 A:Map position: 3

Query Match 76.2%; Score 32; DB 2; Length 264;
 Best Local Similarity 55.6%; Pred. No. 71;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLKDDLEA 9
 |||||
 Db 26 VLKDDLEA 34

RESULT 14

A64988
 hypothetical 37.8 kD protein in rply-proL intergenic region - Escherichia coli (strai
 C:Species: Escherichia coli
 C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
 C:Accession: A64988
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617
 A:Accession: A64988
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-335 <BLAT>
 A:Cross-references: GB:AE000308; GB:U00096; NID:gl788508; PIDN:AAC75247.1; PID:gl788;
 A:Experimental source: strain K-12, substrain MG1655
 C:Genetics:

RESULT 6
S43048
polyketide synthase type I - Streptomyces antibioticus
N:Contains: acyl carrier protein; acyltransferase; ketoreductase; thio-
C:Species: Streptomyces antibioticus
C:Date: 13-Jan-1995 #sequence_revision 06-Dec-1996 #text_change 26-May-2000
C:Accession: S43048; S41729
R:Swan, D.G.; Rodriguez, A.M.; Vilches, C.; Mendez, C.; Salas, J.A.
submitted to the EMBL Data Library, February 1993
A:Reference number: S43048
A:Accession: S43048
A:Molecule type: DNA
A:Residues: 1-3519 <SWA>
A:Cross-references: EMBL:109654; NID:g153407; PIDN:AAA19695.1; PID:g153408
R:Swan, D.G.; Rodriguez, A.M.; Vilches, C.; Mendez, C.; Salas, J.A.
Mol. Gen. Genet. 242, 358-362, 1994
A:Title: Characterisation of a Streptomyces antibioticus gene encoding a type I polyketide
A:Reference number: S41729; MUID:94150470
A:Accession: S41729
A:Molecule type: DNA
A:Status: nucleic acid sequence not shown
A:Residues: 1683-3238, 3273-3303, 'K', 3305-3407, 'T', 3409-3462, 'Y', 3464-3516, 'E', 3518-3519
A:Cross-references: EMBL:109654
C:Genetics:
A:Start codon: GTG
C:Superfamily: [acyl-carrier-protein] S-malonyltransferase homology; 3-oxoacyl-[acyl-car-
ogy; short-chain alcohol dehydrogenase homology
C:Keywords: antibiotic biosynthesis; carrier protein
F:59-462/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS1>
F:570-851/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT1>
F:1202-1381/Domain: short-chain alcohol dehydrogenase homology <SAD1>
F:1489-1560/Domain: acyl carrier protein homology <ACP1>
F:1708-2111/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS2>
F:2221-2502/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT2>
F:2858-3037/Domain: short-chain alcohol dehydrogenase homology <SAD2>
F:3143-3214/Domain: acyl carrier protein homology <ACP2>
F:3305-3500/Domain: oleoyl-[acyl-carrier-protein] hydrolase homology <ACPH>

Query Match 81.0%; Score 34; DB 2; Length 3519;
Best Local Similarity 87.5%; Pred. No. 4.7e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLEA 9
|||:||||
Db 770 LRDELLEA 777

RESULT 7
D83714
surface adhesin A precursor psaa [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000
C:Accession: D83714
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20263314
A:Accession: D83714
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-300 <STO>
A:Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BA804235.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: psaa
C:Superfamily: adhesin B

Query Match 78.6%; Score 33; DB 2; Length 300;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLRDDLE 8
|:||||:
Db 144 VIRDDLVE 151

RESULT 8
T11672
quinone oxidoreductase homolog - cowpea
C:Species: Vigna unguiculata (cowpea)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C:Accession: T11672
R:Krause, A.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z17311
A:Accession: T11672
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-324 <KRA>
A:Cross-references: EMBL:Y08624
A:Experimental source: cultivar red caloona; root hair
C:Genetics:
A:Gene: Ted2
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
F:26-314/Domain: long-chain alcohol dehydrogenase homology <LAD>

Query Match 78.6%; Score 33; DB 2; Length 324;
Best Local Similarity 77.8%; Pred. No. 56;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLRDDLEA 9
|:||||:
Db 270 VIRDELLEA 278

RESULT 9
H85073
probable transposon protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C:Accession: H85073
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold St
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488
A:Accession: H85073
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-483 <STO>
A:Cross-references: GB:NC_001268; NID:g7267351; PIDN:CAB81124.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4g07540
A:Map position: 4

Query Match 78.6%; Score 33; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLRDDLL 7
|:||||:
Db 145 VLRDDLL 151

RESULT 10
I38728
epidermal growth factor receptor kinase substrate - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jun-2000
C:Accession: I38728
R:Wond, W.T.; Carlomagno, F.; Druck, T.; Barletta, C.; Croce, C.M.; Huebner, K.; Krau
Oncogene 9, 3057-3061, 1994

DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE C-TERMINAL SEQUENCE OF ORF C PRODUCT SHOWS HOMOLOGY TO SEVERAL
 DE BACTERIAL ORFS.
 OS Leishmania donovani.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5661;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MHOM/BL/67/ITMAP263;
 RX MEDLINE=95047425; PubMed=7958944;
 RA Myler P.J., Venkataraman G.M., Lodes M.J., Stuart K.D.;
 RT "A frequently amplified region in Leishmania contains a gene conserved
 RT in prokaryotes and eukaryotes."
 RL Gene 148:187-193(1994).
 DR EMBL; U02459; AAA64631.1; -.
 DR InterPro; IPR000613; -.
 DR Pfam; PF00849; Pseudo0_synth_2; 1.
 DR ProDom; PD001819; -; 1.
 DR PROSITE; PS01129; PSI_RLU; 1.
 SQ SEQUENCE 741 AA; 80060 MW; AE28C60ABDFC6C72 CRC64;
 Query Match 75.6%; Score 34; DB 5; Length 741;
 Best Local Similarity 62.5%; Pred. No. 3e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LHDDLEA 9
 DB 628 LHDDIIDA 635
 RESULT 9
 ID Q9NDK7 PRELIMINARY; PRT; 741 AA.
 AC Q9NDK7;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE 511.8.
 GN 511.8.
 OS Leishmania major.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIEDLIN;
 RA Myler P.J., Sisk E., Hixson G., Kiser P., Rickel E., Hassebrock M.,
 RA Cavthra J., Marsolini F., Sunkin S., Stuart K.D., Cunningham M.,
 RA Beverley S.; (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC005801; AAF77202.1; -.
 DR InterPro; IPR000345; -.
 DR InterPro; IPR000613; -.
 DR InterPro; IPR002990; -.
 DR Pfam; PF00849; Pseudo0_synth_2; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 DR PROSITE; PS01129; PSI_RLU; 1.
 SQ SEQUENCE 741 AA; 79890 MW; 81AE04A9B109A3F2 CRC64;
 Query Match 75.6%; Score 34; DB 5; Length 741;
 Best Local Similarity 62.5%; Pred. No. 3e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LHDDLEA 9
 DB 628 LHDDIIDA 635
 RESULT 10.

Q9VA13 PRELIMINARY; PRT; 774 AA.
 ID Q9VA13;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE CG11318 PROTEIN.
 GN CG11318.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champen M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.R.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Harris A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.D., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003776; AAF57115.1; -.
 DR FlyBase; FBgn0039818; CG11318.
 DR InterPro; IPR000203; -.
 DR InterPro; IPR000832; -.
 DR Pfam; PF00002; 7tm.2; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00303; GPS; 1
 SQ SEQUENCE 774 AA; 87359 MW; 0C3FF3A99A12CF79 CRC64;
 Query Match 75.6%; Score 34; DB 5; Length 774;
 Best Local Similarity 85.7%; Pred. No. 3.2e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LHDDLEA 8
 DB 121 LHDDVLE 127

RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., DuBois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jivani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noilting J., Reeve J.N.,
RA "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
DR EMBL; AE000868; AAB85440.1; -;
DR InterPro; IPR002052; -;
DR InterPro; IPR003356; -;
DR Pfam; PF02384; N6_Mtase; 1;
DR PRINTS; PR00507; N12N6WTFRASE;
DR PROSITE; PS00092; NG_MTASE; UNKNOWN_1;
SQ SEQUENCE 616 AA; 71715 MW; 06D4F1076A5D58AD CRC64;

Query Match 77.8%; Score 35; DB 1; Length 616;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
DB 465 VLEDDLLEA 473

RESULT 6
ID Q9V966 PRELIMINARY; PRT; 332 AA.
AC Q9V966;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE CG9025 PROTEIN.
GN Drosophila melanogaster (Fruit fly).
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Calle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.T., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fiesler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Hock J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matti B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclit J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reibert C., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003791; AAF57431.1; -;
DR HSSP; P55273; 18D8
DR FlyBase; FBgn0034542; CG9025.
DR InterPro; IPR002110; -;
DR Pfam; PF00023; ank; 5;
DR PROSITE; PS50088; ANK_REPEAT; 3;
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1;
DR SMART; SM00248; ANK; 1;
SQ SEQUENCE 332 AA; 36359 MW; DD6F2CD87C66186E CRC64;

Query Match 75.6%; Score 34; DB 5; Length 332;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHDDLLEA 9
DB 285 LHEDVLEA 292

RESULT 7
ID Q9NKM2 PRELIMINARY; PRT; 640 AA.
AC Q9NKM2;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE 511.8 (FRAGMENT).
GN 511.8.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Myler P.J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC009603; AAF70540.1; -;
DR InterPro; IPR000345; -;
DR InterPro; IPR000613; -;
DR InterPro; IPR002990; -;
DR Pfam; PF00849; Pseudou-synth_2; 1;
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1;
DR PROSITE; PS01129; PSI_RLU; 1;
DR NON_TER 640
SQ SEQUENCE 640 AA; 68503 MW; 8A19583709E1BB7D CRC64;

Query Match 75.6%; Score 34; DB 5; Length 640;
Best Local Similarity 62.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHDDLLEA 9
DB 628 LHDDIIDA 635

RESULT 8
ID Q25257 PRELIMINARY; PRT; 741 AA.
AC Q25257;

Best Local Similarity 66.7%; Pred. No. 5.9e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLEA 9
DB 160 VVHSDMLEA 168

RESULT 12

Q99387 ID Q99387 PRELIMINARY; PRT; 145 AA.
AC Q99387
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE HYPOTHETICAL 16 KDA PROTEIN (ORF145).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
ON NCBI_TaxID=1280;
RX [1]
RC SEQUENCE FROM N.A.
RC STRAIN=NTC 8325 / ISOLATE BB270;
RX MEDLINE=91033056; PubMed=2227446;
RA Ryffel C., Tesch W., Birch-Machin I., Reynolds P.E.,
RA Barberis-Maino L., Kayser F.H., Berger-Baechli B.;
RT "Sequence comparison of mecA genes isolated from methicillin-resistant
RT Staphylococcus aureus and Staphylococcus epidermidis.";
RL Gene 94:137-138(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NTC 8325;
RX MEDLINE=92041850; PubMed=1718947;
RA Ryffel C., Bucher R., Kayser F.H., Berger-Baechli B.;
RT "The Staphylococcus aureus mec determinant comprises an unusual
RT cluster of direct repeats and codes for a gene product similar to the
RT Escherichia coli sn-glycerophosphoryl diester phosphodiesterase.";
RL J. Bacteriol. 173:7416-7422(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BMS-1 / BB270;
RX MEDLINE=98101461; PubMed=9440511;
RA Wu S., de Lencastre H., Tomas A.;
RT "Genetic organization of the mecA region in methicillin-susceptible
RT and methicillin-resistant strains of Staphylococcus sciuri.";
RL J. Bacteriol. 180:236-242(1998).
DR EMBL; X52594; CAA36830.1;
DR EMBL; Y14051; CAA74379.1;
KW Hypothetical protein.
SQ SEQUENCE 145 AA; 16286 MW; 689022117880DCE4 CRC64;

Query Match 73.3%; Score 33; DB 2; Length 145;
Best Local Similarity 62.5%; Pred. No. 85;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLE 8
DB 48 IHHDDYLE 55

RESULT 13

Q94256 ID Q94256 PRELIMINARY; PRT; 174 AA.
AC Q94256;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE COSMID K04A8.
GN K04A8.9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.

Query Match 75.6%; Score 34; DB 5; Length 1383;

RESULT 11
Q9VDA0 ID Q9VDA0 PRELIMINARY; PRT; 1383 AA.
AC Q9VDA0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE CG7922 PROTEIN.
GN CG7922.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
ON NCBI_TaxID=7227;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.G., Worley J.P., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.C., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Barker E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Adayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glöck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -!- SIMILARITY: TO DEAD/DEAH BOX HELICASE FAMILY.
CC -!- SIMILARITY: TO HELICASE C-TERMINAL DOMAIN.
DR EMBL; AE003735; AAF55897.1;
DR FlyBase; FBgn0038889; CG7922.
DR InterPro; IPR000531;
DR InterPro; IPR001410;
DR InterPro; IPR001650;
DR Pfam; PF00270; DEAD_1.
DR Pfam; PF00271; helicase_C_1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
DR SMART; SM00487; DEXDC; 1.
KW ATP-binding; Helicase.
SQ SEQUENCE 1383 AA; 157452 MW; 6B19A6FD554AD88E CRC64;

OX NCBI_TaxID=6239;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Aliscough R., Anderson K., Baynes C., Berks M., Coulson A.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fulton L.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kerhaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
 RA Smaildon N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RN Nature 368:32-38(1994).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Geisel C., Bradshaw H.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U64849; AAC48055.1; -;
 DR InterPro: IPR000004; -;
 DR SMART: SM00118; SAPB; 1;
 SQ SEQUENCE 174 AA; 19210 MW; A6303CF6383BEBD9 CRC64;

Query Match 73.3%; Score 33; DB 5; Length 174;
 Best Local Similarity 77.8%; Pred. No. 1e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
 || |||||
 Db 129 VLKDDLLEA 137

RESULT 14

Q9RPT9 PRELIMINARY; PRT; 175 AA.
 AC Q9RPT9;
 DT 01-MAY-2000 (TREMELrel. 13, Created)
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMELrel. 14, Last annotation update)
 DE HYPOTHETICAL 20.3 KDA PROTEIN.
 OS Streptomyces albus.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC21838;
 RA Kwon H.-J., Lee S.-Y., Hong S.-K., Park U.-W., Suh J.-W.;
 RT "Heterologous Expression of Streptomyces albus Genes Linked to an
 Integrating Element and Activation of Antibiotic Production.";
 RL J. Microbiol. Biotechnol. 9:488-497(1999).
 DR EMBL: AF145724; AAD46513.1; -;
 DR InterPro: IPR000182; -;
 DR Pfam: PF00583; Acetyltransf. 1.
 KW Hypothetical protein.
 SQ SEQUENCE 175 AA; 20300 MW; 22A46EA40732DFOA CRC64;

Query Match 73.3%; Score 33; DB 2; Length 175;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDLLE 8
 |||||
 Db 33 HDLLE 18

RESULT 15

Q9S3K5 PRELIMINARY; PRT; 210 AA.
 AC Q9S3K5;
 DT 01-MAY-2000 (TREMELrel. 13, Created)
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMELrel. 13, Last annotation update)
 DE GLYCEROPHOSPHORYLDIESTER PHOSPHODIESTERASE (FRAGMENT).
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON-TN55X;
 RX MEDLINE=99278010; PubMed=10348769;
 RA Ito T., Katayama Y., Hiramatsu K.;
 RT "cloning and nucleotide sequence determination of the entire mec DNA
 RT of pre-methicillin-resistant Staphylococcus aureus N315.";
 RL Antimicrob. Agents Chemother. 43:1449-1458(1999).
 DR EMBL: D86934; BAA82224.1; -;
 FT NON_TER 1
 SQ SEQUENCE 210 AA; 23757 MW; 3F0B88A13397D668 CRC64;

Query Match 73.3%; Score 33; DB 2; Length 210;
 Best Local Similarity 62.5%; Pred. No. 1.3e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLLE 8
 :||| |
 Db 48 ITHDDVLE 55

Search completed: July 10, 2001, 08:36:07
 Job time: 260 sec

A:Gene: yejK

Query Match 76.2%; Score 32; DB 2; Length 335;
Best Local Similarity 87.5%; Pred. No. 92;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLRDLDLLE 8
 |||||
DB 24 VLRDLSLLE 31

RESULT 15

H85857

hypothetical protein yejK [imported] - Escherichia coli (strain O157:H7)

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001

C:Accession: H85857

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: H85857

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-335 <STO>

A:Cross-references: GB:AF005174; NID:2516518; PIDN:AAG57324.1; GSPDB:GN00145; UWGP:234

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: yejK

Query Match 76.2%; Score 32; DB 2; Length 335;
Best Local Similarity 87.5%; Pred. No. 92;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLRDLDLLE 8
 |||||
DB 24 VLRDLSLLE 31

Search completed: July 10, 2001, 08:31:41
Job time: 210 sec

Db 48 IHHDDYLE 55
::||| ||

RESULT 8

T44122
probable glycerophosphodiester phosphodiesterase (EC 3.1.4.46) [imported] - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 11-May-2000
C:Accession: T44122
R:Ito, T.; Katayama, Y.; Hiramatsu, K.
Antimicrob. Agents Chemother. 43, 1449-1458, 1999
A:Title: Cloning and nucleotide sequence determination of the entire mec DNA of pre-methicillin-resistant *Staphylococcus aureus* strain N315
A:Reference number: 222733; MUID:99278010
A:Accession: T44122
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-210 <IT0>
A:Cross-references: EMBL:D86934; PIDN:BAA82224.1
A:Experimental source: strain N315
C:Keywords: phosphoric diester hydrolase

Query Match 73.3%; Score 33; DB 2; Length 210;
Best Local Similarity 62.5%; Pred. No. 54;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLE 8
::||| ||

Db 48 IHHDDYLE 55

RESULT 9

S76860
hypothetical protein sll1549 - *Synechocystis* sp. (strain PCC 6803)
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S76860
O:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
R.Kane, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.
A:Reference number: S74322; MUID:97061201
A:Accession: S76860
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-238 <KAN>
A:Cross-references: EMBL:D90917; GB:AB001339; NID:gl653836; PIDN:BAA18772.1; PID:d101950
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 73.3%; Score 33; DB 2; Length 238;
Best Local Similarity 85.7%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HDLLEA 9
::||| ||

Db 193 HDLLEA 199

RESULT 10

GB2601
conserved hypothetical protein XF2090 [imported] - *Xylella fastidiosa* (strain 9a5c)
C:Species: *Xylella fastidiosa*
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
R:Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequence
C:Accession: GB2601
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
A:Reference number: AB2515; MUID:20365717
A:Note: for a complete list of authors see reference number A59328 below

A:Accession: G82601
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-259 <SIM>
A:Cross-references: GB:AE004024; GB:AE003849; NID:g9107208; PIDN:AAF84889.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF2090

Query Match 73.3%; Score 33; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDLLE 8
::||| ||

Db 82 HDLLE 87

RESULT 11

DB3371
probable dehydrogenase PA2199 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: DB3371
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pa
A:Reference number: AB2950; MUID:20437337
A:Accession: DB3371
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-291 <STO>
A:Cross-references: GB:AE004646; GB:AE004091; NID:g9948213; PIDN:AAG05587.1; GSPDB:G
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2199

Query Match 73.3%; Score 33; DB 2; Length 291;
Best Local Similarity 77.8%; Pred. No. 78;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLEA 9
::||| |||

Db 259 LLHDDVLEA 267

RESULT 12

B75457
polyphenyl synthase - *Deinococcus radiodurans* (strain R1)
C:Species: *Deinococcus radiodurans*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: B75457
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.

A:Reference number: A75250; MUID:20036896

A:Accession: B75457

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-320 <WHI>

A:Cross-references: GB:AE001946; GB:AE000513; NID:g6458655; PIDN:AAF10509.1; PID:g645865

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR0932

A:Map position: 1

C:Superfamily: prenyl transferase A

Query Match 73.3%; Score 33; DB 2; Length 320;
Best Local Similarity 62.5%; Pred. No. 86;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHDDLL 8

:|||||:

Db 79 LLHDDLLD 86

RESULT 13

C83075

Octaprenyl-diphosphate synthase PA4569 [imported] - *Pseudomonas aeruginosa* (strain PA01)

C:Species: *Pseudomonas aeruginosa*

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: C83075

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337

A:Accession: C83075

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-322 <STO>

A:Cross-references: GB:AF004870; GB:AE004091; NID:g9950807; PIDN:AA07957.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: ispB; PA4569

C:Superfamily: prenyl transferase A

Query Match 73.3%; Score 33; DB 2; Length 322;

Best Local Similarity 55.6%; Pred. No. 87;

Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHDDLL 9

:|||||:

Db 81 LLHDDVDA 89

RESULT 14

A45251

DNA-directed DNA polymerase (EC 2.7.7.7) III delta chain - *Escherichia coli*

C:Species: *Escherichia coli*

C>Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999

C:Accession: A45251; A46738; F64798

R:Carter, J.R.; Franden, M.A.; Aebersold, R.; McHenry, C.S.

J. Bacteriol. 174, 7013-7025, 1992

A:Title: Molecular cloning, sequencing, and overexpression of the structural gene encodi

A:Reference number: A45251; MUID:93015766

A:Accession: A45251

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-343 <CAR>

A:Cross-references: GB:M94267; NID:g145784; PIDN:AAB59047.1; PID:g145785

A:Note: sequence extracted from NCBI backbone (NCBIP:117007)

R:Dong, Z.; Onrust, R.; Skangalis, M.; O'Donnell, M.

J. Biol. Chem. 268, 11758-11765, 1993

A:Title: DNA polymerase III accessory proteins. I. holo and holoB encoding delta and

A:Reference number: A46738; MUID:93280136

A:Accession: A46738

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-343 <DON>

A:Cross-references: GB:L04576; NID:g145728; PIDN:AAA23675.1; PID:g145729

A:Experimental source: strain K-12

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.,

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of *Escherichia coli* K-12.

A:Reference number: A64720; MUID:97426617

A:Accession: F64798

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-343 <BLAT>

A:Cross-references: GB:AE000168; GB:U00096; NID:g1786849; PIDN:AAC73741.1; PID:g17868

A:Experimental source: strain K-12, substrain MG1655

C:Genetics:

A:Gene: holoA

C:Complex: DNA polymerase III is a multichain complex; alpha, epsilon, theta, tau, ga

C:Function: <GEN>

A:Description: DNA synthesis; synthesizes both, the lagging and the leading strands

A:Pathway: DNA biosynthesis

A:Note: core enzyme (catalytic core) contains chains alpha, epsilon and theta; alpha

required for assembly; tau allows dimerization of the core complex and processivity

ts; the holoenzyme is completed by addition of beta chain which clamps the enzyme to

C:Function:

A:Description: delta chain seems to interact with the gamma chain

A:Note: gamma/delta complex is composed of chains gamma, delta, delta', psi and chi

C:Keywords: DNA biosynthesis; DNA replication; nucleotidyltransferase

Query Match 73.3%; Score 33; DB 2; Length 343;

Best Local Similarity 85.7%; Pred. No. 93;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHDDLL 7

:|||||:

Db 103 LLHDDLL 109

RESULT 15

B85564

DNA polymerase III, delta subunit [imported] - *Escherichia coli* (strain O157:H7)

C:Species: *Escherichia coli*

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001

C:Accession: B85564

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimantanta, E.; Potamousis, K.; Apoda

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: B85564

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-343 <STO>

A:Cross-references: GB:AE005174; NID:g12513544; PIDN:AAG54974.1; GSPDB:GN00145; UWGP

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: holoA

Query Match 73.3%; Score 33; DB 2; Length 343;

Best Local Similarity 85.7%; Pred. No. 93;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHDDLL 7

:|||||:

Db 103 LLHDDLL 109

us-09-489-760-2.rpr

Tue Jul 10 13:30:14 2001

Search completed: July 10, 2001, 08:31:41
Job time: 210 sec

7

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 10, 2001, 08:31:17 ; Search time 12.64 Seconds

(without alignments)
24.391 Million cell updates/sec

Title: US-09-489-760-2

Perfect score: 45

Sequence: 1 VLHDDLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	35	77.8	603	1	VEL_HPV21	P50759	human papill
2	35	77.8	604	1	VEL_HPV19	Q02048	human papill
3	35	77.8	605	1	VEL_HPV14	P36721	human papill
4	34	75.6	130	1	CHEV_CAMJE	P71129	campylobact
5	33	73.3	343	1	HOLA_ECOLI	P28630	escherichia
6	33	73.3	397	1	UL50_HCMVA	P16791	human cytom
7	33	73.3	443	1	MDM1_YEAST	Q01846	saccharomyc
8	33	73.3	519	1	CP5V_CANAP	P43083	candida api
9	33	73.3	519	1	CP5W_CANAP	Q12573	candida api
10	33	73.3	604	1	VEL_HPV25	Q02049	human papill
11	33	73.3	653	1	YDCP_ECOLI	P76104	escherichia
12	33	73.3	1770	1	R115_YEAST	P43565	saccharomyc
13	32	71.1	107	1	RLAL_CHLRE	P29763	chlamydomon
14	32	71.1	166	1	YVAE_VACCC	P20514	vaccinia vi
15	32	71.1	245	1	B2LF_EBV	P03206	epstein-bar
16	32	71.1	284	1	THT3_MYCTU	Q59570	mycobacteri
17	32	71.1	296	1	Y842_CAEEL	Q09371	caenorhabdi
18	32	71.1	410	1	YCAQ_ECOLI	P75843	escherichia
19	32	71.1	736	1	KPCE_RABIT	P10830	oryctolagus
20	32	71.1	737	1	KPCE_HUMAN	Q02156	homo sapien
21	32	71.1	737	1	KPCE_MOUSE	P16054	mus musculus
22	32	71.1	737	1	KPCE_RAT	P09216	rattus norv
23	32	71.1	743	1	KPC2_APLCA	Q16975	aplysia cal
24	32	71.1	767	1	DLG4_HUMAN	P78352	homo sapien
25	31.5	70.0	549	1	YQCE_ECOLI	P32703	escherichia
26	31	68.9	103	1	RLAL_POLPE	P27464	polyorchis
27	31	68.9	149	1	LRPB_BACSU	P96653	bacillus su
28	31	68.9	231	1	YHHW_ECOLI	P46852	escherichia
29	31	68.9	247	1	UGPO_ECOLI	P10908	escherichia
30	31	68.9	290	1	ARY1_HUMAN	P18440	homo sapien
31	31	68.9	428	1	DGTP_MYCSM	O52199	mycobacteri
32	31	68.9	469	1	K64_HUMAN	Q92504	homo sapien
33	31	68.9	499	1	AMPA_CHLPN	Q928f8	chlamydia p

34	31	68.9	584	1	HEMA_INBLE	P03460	influenza b
35	31	68.9	586	1	VDME_BPT3	P10310	bacterioph
36	31	68.9	604	1	VEL_HPV12	Q05134	human papil
37	31	68.9	604	1	VEL_HPV36	P50808	human papil
38	31	68.9	605	1	VEL_HPV20	P50758	human papil
39	31	68.9	605	1	VEL_HPV47	P22419	human papil
40	31	68.9	606	1	VEL_HPV05	P06920	human papil
41	31	68.9	606	1	VEL_HPV5B	P26542	human papil
42	31	68.9	606	1	VEL_HPV7	O40619	human papil
43	31	68.9	688	1	YQAQ_SCHPO	Q10109	schizosacch
44	31	68.9	727	1	KDGA_RAT	P51556	rattus norv
45	31	68.9	730	1	KDGA_MOUSE	O88673	mus musculu

ALIGNMENTS

RESULT 1
VEL_HPV21
ID VEL_HPV21 STANDARD; PRT; 603 AA.
AC P50759;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE REPLICATION PROTEIN E1.
GN E1.
OS Human papillomavirus type 21.
OC Viruses; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
OX NCBI_TaxID=31548;
RN [1]
RP SEQUENCE FROM N.A.
RA Delius H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF
CC VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2
CC PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH
CC CONTAINS BINDING SITES FOR BOTH PROTEINS.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.

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CC -----
CC EMBL: U31779; AAA79396.1; -
CC InterPro: IPR001177; -
CC Pfam: PF00519; E1; 1.
CC Pfam: PF00524; E1; 1.
CC Early protein; DNA replication; Helicase; ATP-binding; DNA-binding;
CC Nuclear protein.
CC NP_BIND 431 438
CC FT NP_BIND 431 438
CC SEQUENCE 603 AA; 68983 MW; 93006494BEF10339 CRC64;

Query Match 77.8%; Score 35; DB 1; Length 603;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 2 LHHDDLEA 9
Db 200 VHHDDLES 207
:|||||:

RESULT 2
VEL_HPV19
ID VEL_HPV19 STANDARD; PRT; 604 AA.
AC Q02048;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE GN REPLICATION PROTEIN E1.
 OS Human papillomavirus type 19.
 OC Viruses; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
 OX NCBI_TaxID=10606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94265501; PubMed=8205838;
 RA Delius H., Hofmann B.;
 RT "Primer-directed sequencing of human papillomavirus types.";
 RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
 RN [2]
 RP SEQUENCE OF 331-382 FROM N.A.
 RX MEDLINE=92407963; PubMed=1326639;
 RA Chan S.Y., Bernard H.U., Ong C.K., Chan S.P., Birgit H., Delius H.;
 RT "Phylogenetic analysis of 48 papillomavirus types and 28 subtypes and
 variants: a showcase for the molecular evolution of DNA viruses.";
 RL J. Virol. 66:5714-5725(1992).
 CC -1- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF
 CC VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2
 CC PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH
 CC CONTAINS BINDING SITES FOR BOTH PROTEINS.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
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 DR EMBL; X74470; CAA52520.1; -;
 DR EMBL; M96320; AAA47009.1; -;
 DR PIR; S36487; S36487;
 DR InterPro: IPR001177; -;
 DR Pfam; PF00519; El; 1.
 DR Pfam; PF00524; El_N; 1.
 DR Early protein; DNA replication; Helicase; ATP-binding; DNA-binding;
 KW Nuclear protein.
 FT NP_BIND 432 439 ATP (POTENTIAL).
 SQ SEQUENCE 604 AA; 69153 MW; 6CC7376D631D3FA1 CRC64;

Query Match 77.8%; Score 35; DB 1; Length 604;
 Best Local Similarity 75.0%; Pred. No. 23;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LHDDLLEA 9
 :|||||:
 DB 201 VHDDLLES 208

RESULT 3
 VEL_HPV14
 ID VEL_HPV14 STANDARD; PRT; 605 AA.
 AC P36721.
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE REPLICATION PROTEIN E1.
 GN E1.
 OS Human papillomavirus type 14.
 OC Viruses; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
 OX NCBI_TaxID=10605;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94265501; PubMed=8205838;
 RA Delius H., Hofmann B.;
 RT "Primer-directed sequencing of human papillomavirus types.";
 RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
 CC -1- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF
 CC VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2

CC PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH
 CC CONTAINS BINDING SITES FOR BOTH PROTEINS.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
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 DR EMBL; X74467; CAA52502.1; -;
 DR PIR; S36469; S36469.
 DR InterPro: IPR001177; -;
 DR Pfam; PF00519; El; 1.
 DR Pfam; PF00524; El_N; 1.
 DR Early protein; DNA replication; Helicase; ATP-binding; DNA-binding;
 KW Nuclear protein.
 FT NP_BIND 433 440 ATP (POTENTIAL).
 SQ SEQUENCE 605 AA; 69302 MW; 6702915505AA6491 CRC64;

Query Match 77.8%; Score 35; DB 1; Length 605;
 Best Local Similarity 75.0%; Pred. No. 23;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LHDDLLEA 9
 :|||||:
 DB 202 VHDDLLES 209

RESULT 4
 CHEY_CAMJE
 ID CHEY_CAMJE STANDARD; PRT; 130 AA.
 AC P71129;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CHEMOTAXIS PROTEIN CHEY HOMOLOG.
 GN CHEY OR CJ1118C.
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
 OC Campylobacter.
 OX NCBI_TaxID=197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCTC 11828;
 RA Marchant J.E., Henderson J., Wren B.W., Ketley J.M.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=81116;
 RA MEDLINE=98386495; PubMed=9720026;
 RA Fry B.N., Korolik V., ten Brinke J.A., Pennings M.T.T., Zalm R.,
 RA Teunis B.J.J., Coloe P.J., van der Zeijst B.A.M.;
 RT "The lipopolysaccharide biosynthesis locus of Campylobacter jejuni
 81116.";
 RL Microbiology 144:2049-2061(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCTC 11168;
 RA MEDLINE=20150912; PubMed=10688204;
 RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
 RA Bigham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
 RA Jagers K., Karylshev A.V., Moule S., Pallen M.J., Penn C.W.,
 RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
 RA Whitehead S., Barrell B.G.;
 RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
 reveals hypervariable sequences.";
 RL Nature 403:665-668(2000).
 RN [4]
 RP SEQUENCE OF 12-130 FROM N.A.


```

RC STRAIN=ATCC 55026 / 81-176;
RX MEDLINE=97231343; PubMed=6738;
RA YAO R., BURR D.H., GUERRY P.;
RT "Chey-mediated modulation of Campylobacter jejuni virulence.";
RL MOL. Microbiol. 23:1021-1032(1997).
CC -!- FUNCTION: INVOLVED IN THE TRANSMISSION OF SENSORY SIGNALS FROM
CC THE CHEMORECEPTORS TO THE FLAGELLAR MOTORS. CHEY SEEMS TO REGULATE
CC THE CLOCKWISE (CW) ROTATION (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE RESPONSE REGULATORY FAMILY.
CC -----
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CC -----
DR EMBL: U75208; AAB17571.1; -
DR EMBL: Y11648; CAA72347.1; -
DR EMBL: AL139077; CAB73373.1; -
DR EMBL: U62038; AAC44858.1; -
DR HSSP: P06143; ICYF
DR InterPro: IPR001789; -
DR Pfam: PF00072; response_reg; 1.
KW Chemotaxis; Sensory transduction; Phosphorylation; Flagellar rotation.
FT DOMAIN 1 119 RECEIVER DOMAIN (POTENTIAL).
FT MOD_RES 53 53 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 130 AA; 14437 MW; 41634D8ADE6C5081 CRC64;

Query Match 75.68; Score 34; DB 1; Length 130;
Best Local Similarity 85.78; Pred. No. 6.3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDDLLEA 9
| | | | |
DB 25 HDDVLEA 31

RESULT 5
HOLA_ECOLI
ID HOLA_ECOLI STANDARD; PRT; 343 AA.
AC P28630;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE "DNA POLYMERASE III, DELTA SUBUNIT (EC 2.7.7.7)."
GN HOLA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=93280136; PubMed=8505303;
RA Dong Z., Onrust R., Skangalis M., O'Donnell M.;
RT "DNA polymerase III accessory proteins. I. hola and holaB encoding
RT delta and delta'.";
RL J. Biol. Chem. 268:11758-11765(1993).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=MAF102;
RX MEDLINE=93015766; PubMed=1400251;
RA Carter J.R., Franden M.A., Aebersold R.H., McHenry C.S.;
RT "Molecular cloning, sequencing, and overexpression of the structural
RT gene encoding the delta subunit of Escherichia coli DNA polymerase
RT III holoenzyme.";
RL J. Bacteriol. 174:7013-7025(1992).
RN [3]
RP SEQUENCE FROM N.A.

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```

RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [4]
RP SEQUENCE FROM N.A.
RA Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
RA Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
RA Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RN [6]
RP PRELIMINARY SEQUENCE OF 1-49 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=88058785; PubMed=3316191;
RA Takase I., Ishino F., Wachi M., Kamata H., Doi M., Asoh S.,
RA Matsuzawa H., Ohta T., Matsubashi M.;
RT "Genes encoding two lipoproteins in the leuS-dacA region of the
RT Escherichia coli chromosome.";
RL J. Bacteriol. 169:5692-5699(1987).
RN [7]
RP CHARACTERIZATION.
RX MEDLINE=93280137; PubMed=8505304;
RA Onrust R., O'Donnell M.;
RT "DNA polymerase III accessory proteins. II. Characterization of delta
RT and delta'.";
RL J. Biol. Chem. 268:11766-11772(1993).
RN [8]
RP REVIEW.
RX MEDLINE=92246902; PubMed=1575709;
RA O'Donnell M.;
RT "Accessory protein function in the DNA polymerase III holoenzyme from
RT E. coli.";
RL Bioessays 14:105-111(1992).
CC -!- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
CC RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
CC THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
CC THE DELTA SUBUNIT SEEMS TO INTERACT WITH THE GAMMA SUBUNIT TO
CC TRANSFER THE BETA SUBUNIT ON THE DNA.
CC -!- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE =
CC N PYROPHOSPHATE + DNA(N).
CC -!- SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA
CC CHAINS) THAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOW THE CORE
CC DIMERIZATION TO FORM THE POLIII' COMPLEX. POLIII' ASSOCIATES WITH
CC THE GAMMA COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA', PSI,
CC AND CHI) AND WITH THE BETA CHAIN. THE FINAL COMPOSITION OF THE
CC COMPLEX IS: (ALPHA,EPSILON,THETA)[2]-TAU[2]-(GAMMA,DELTA,DELTA',
CC PSI,CHI)[2]-BETA[4]
CC -----
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CC -----

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DR EMBL; L04576; AAA23675.1; -
DR EMBL; M94267; AAB59047.1; -
DR EMBL; AE000168; AAC73741.1; -
DR EMBL; U82598; AAB40841.1; -
DR EMBL; D90704; BAA35287.1; -
DR EMBL; M18277; -; NOT_ANNOTATED_CDS.
DR PIR; A45251; A45251.
DR PIR; A46738; A46738.
DR ECO2DBASE; F032.4; 6TH EDITION.
DR Ecogene; EG11412; hola.
KW Transferase; DNA-directed DNA polymerase; DNA replication.
SQ SEQUENCE 343 AA; 38703 MW; 87239A678FE16BE2 CRC64;

Query Match 73.3%; Score 33; DB 1; Length 343;
Best Local Similarity 85.7%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHDDL 7
DB 103 LLHDDL 109

RESULT 6
UL50_HCMVA STANDARD; PRT; 397 AA.
AC P16791;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE PROTEIN UL50.
GN UL50.
OS Human cytomegalovirus (strain AD169).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10360;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90269039; Pubmed=2161319;
RA Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
RA Horsnell T., Hutchinson C.A. III, Kouzarides T., Martignetti J.A.,
RA Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
RA "Analysis of the protein-coding content of the sequence of human
RA Cytomegalovirus strain AD169."
RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL34,
CC HSV-1 26, EBV BFR1, HVS-1 67, HCMV UL50, AND VZV 24.
CC -----
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CC -----
DR EMBL; X17403; CAA35409.1; -
DR PIR; S09813; S09813.
SQ SEQUENCE 397 AA; 42901 MW; 08DC5FA358E8A473 CRC64;

Query Match 73.3%; Score 33; DB 1; Length 397;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
DB 6 VLHDDLVOA 14

RESULT 7
MDM1_YEAST STANDARD; PRT; 443 AA.
ID MDM1_YEAST

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AC Q01846;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE STRUCTURAL PROTEIN MDM1.
GN MDM1 OR YML104C OR YMB339.15C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92332595; Pubmed=1378448;
RA McConnell S.J., Yaffe M.P.;
RA "Nuclear and mitochondrial inheritance in yeast depends on novel
RA cytoplasmic structures defined by the MDM1 protein."
RL J. Cell Biol. 118:385-395(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=S288C / AB972;
RA Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RA Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 190-443 FROM N.A.
RA Stirling C.J.;
RA Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases
CC -1- FUNCTION: ESSENTIAL FOR MITOTIC GROWTH. MEDIANTE ORGANELLE
CC INHERITANCE.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: LOW, TO VIMENTIN AND OTHER INTERMEDIATE FILAMENTS.
CC -1- SIMILARITY: TO S.POMBE SPCC16A11.04.
CC -----
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CC -----
DR EMBL; X66371; CAA47014.1; -
DR EMBL; Z49210; CAA89114.1; -
DR EMBL; X65783; CAA46664.1; -
DR PIR; A42636; A42636.
DR SGD; S0004572; MDM1.
DR InterPro; IPR001683; -
DR Pfam; PF00787; PX; 1.
DR CONFLICT 88 88 Q -> R (IN REF. 1).
FT CONFLICT 215 215 T -> I (IN REF. 1).
FT CONFLICT 379 379 R -> K (IN REF. 1).
FT CONFLICT 397 397 T -> S (IN REF. 1).
FT CONFLICT 412 412 G -> R (IN REF. 1).
SQ SEQUENCE 443 AA; 51470 MW; 9EAA945C8DA70230 CRC64;

Query Match 73.3%; Score 33; DB 1; Length 443;
Best Local Similarity 71.4%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHDDLLE 8
DB 227 MHDDILE 233

RESULT 8
CP5V_CANAP STANDARD; PRT; 519 AA.
ID CP5V_CANAP
AC P43083;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOCHROME P450 52E1 (EC 1.14.14.1) (CYPLIIE1).
GN CYP52E1.

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OS Candida apicola (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=29830;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IMET 43747;
 RX MEDLINE=96367597; PubMed=8771711;
 RA Lottermoser K., Schunck W.H., Asperger O.;
 RT "Cytochromes P450 of the sophorose lipid-producing yeast Candida
 RT apicola: heterogeneity and polymerase chain reaction-mediated cloning
 RT of two genes";
 RL Yeast 12:565-575(1996).
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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 CC
 DR EMBL; X76225; CAA53811.1; -
 DR InterPro; IPR001128; -
 DR InterPro; IPR002402; -
 DR InterPro; IPR002974; -
 DR Pfam; PF00067; p450; 1.
 DR PRINTS; PR00464; EP450II.
 DR PROSITE; PS00086; CYTOCHROME_P450; 1.
 DR Electron transport; Oxidoreductase; Monooxygenase; Heme;
 KW Transmembrane.
 FT TRANSMEM 10 30 POTENTIAL.
 FT TRANSMEM 44 64 POTENTIAL.
 FT BINDING 479 479 HEME (BY SIMILARITY).
 SQ SEQUENCE 519 AA; 58656 MW; 4185235A07EA4370 CRC64;
 Query Match 73.3%; Score 33; DB 1; Length 519;
 Best Local Similarity 75.0%; Pred. No. 47;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLHDDLL 8
 DB 63 MLHDDNLE 70
 RESULT 9
 CP5W_CANAP STANDARD; PRT; 519 AA.
 AC Q12573;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CYTOCHROME P450 52E2 (EC 1.14.14.1) (CYPLIIE2).
 GN CYP52E2.
 OS Candida apicola (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=29830;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IMET 43747;
 RX MEDLINE=96367597; PubMed=8771711;
 RA Lottermoser K., Schunck W.H., Asperger O.;
 RT "Cytochromes P450 of the sophorose lipid-producing yeast Candida
 RT apicola: heterogeneity and polymerase chain reaction-mediated cloning
 RT of two genes";
 RL Yeast 12:565-575(1996).
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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 CC
 DR EMBL; X87640; CAA60980.1; -
 DR InterPro; IPR001128; -
 DR InterPro; IPR002402; -
 DR InterPro; IPR002974; -
 DR Pfam; PF00067; p450; 1.
 DR PRINTS; PR00464; EP450II.
 DR PROSITE; PS00086; CYTOCHROME_P450; 1.
 DR Electron transport; Oxidoreductase; Monooxygenase; Heme;
 KW Transmembrane.
 FT TRANSMEM 10 30 POTENTIAL.
 FT TRANSMEM 44 64 POTENTIAL.
 FT BINDING 461 461 HEME (BY SIMILARITY).
 SQ SEQUENCE 519 AA; 58631 MW; F0B164E22D169C86 CRC64;
 Query Match 73.3%; Score 33; DB 1; Length 519;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HDDLLE 8
 DB 65 HDDLLE 70
 RESULT 10
 VE1_HPV25 STANDARD; PRT; 604 AA.
 ID VE1_HPV25
 AC Q02049;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE REPLICATION PROTEIN E1.
 GN EL.
 OS Human papillomavirus type 25.
 OS Viruses; GSDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
 OX NCBI_TaxID=10609;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94265501; PubMed=8205838;
 RA Delius H., Hofmann B.;
 RT "Primer-directed sequencing of human papillomavirus types";
 RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
 RN [2]
 RP SEQUENCE OF 331-382 FROM N.A.
 RX MEDLINE=92407963; PubMed=1326639;
 RA Chan S.Y., Bernard H.U., Ong C.K., Chan S.P., Birgit H., Delius H.;
 RT "Phylogenetic analysis of 48 papillomavirus types and 28 subtypes and
 RT variants: a showcase for the molecular evolution of DNA viruses";
 RL J. Virol. 66:5714-5725(1992).
 CC -!- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF
 CC VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2
 CC PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH
 CC CONTAINS BINDING SITES FOR BOTH PROTEINS.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC
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 CC
 DR EMBL; X74471; CAA52526.1; -
 DR EMBL; M96321; AAA47010.1; -

DR PIR; S36493; S36493.
 DR InterPro; IPR001177; -.
 DR Pfam; PF00519; E1; 1.
 DR Pfam; PF00524; E1; 1.
 KW Early protein; DNA replication; Helicase; ATP-binding; DNA-binding;
 KW Nuclear protein.
 FT NP_BIND 432 439 ATP (POTENTIAL).
 SQ SEQUENCE 604 AA; 58925 MW; 0A98B84E93B19B9 CRC64;

Query Match 73.3%; Score 33; DB 1; Length 604;
 Best Local Similarity 62.5%; Pred. No. 56;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 LHDDLEA 9
 :||||:|
 Db 201 VHDLLIES 208

RESULT 11
 YDCP_ECOLI
 ID YDCP_ECOLI STANDARD; PRT; 653 AA.
 AC F76104; P76867; P76868; P76865;
 DT 01-NOV-1997 (Rel. 35, Created)
 DE 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PUTATIVE PROTEASE YDCP PRECURSOR (EC 3.4.-.-).
 GN YDCP.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 [1]
 SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 [2]
 SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RA Itoh T., Kasai H., Kimura K., Kimura S., Kitakawa M.,
 RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
 RA Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y.,
 RA Oshima T., Saito N., Sempel G., Seki Y., Sivasubram S.,
 RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
 RA Yamamoto Y., Horiuchi T.;
 RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
 corresponding to the 28.0-40.1 min region on the linkage map.";
 RL DNA Res. 3:363-377(1996).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY U32.

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CC EMBL; A600240; AAC74517.1; AUT_INIT.
 DR EMBL; D90782; BAAL5063.1; -.
 DR EMBL; D90783; BAAL5068.1; -.
 DR EMBL; D90784; BAAL5074.1; -.
 DR EcoGene; EG13759; ydcP.
 DR InterPro; IPR001539; -.
 DR Pfam; PF01136; Peptidase_U32; 1.

DR PROSITE; PS01276; PEPTIDASE_U32; 1.
 KW Hypothetical protein; Hydrolase; Protease; Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 653 PUTATIVE PROTEASE YDCP.
 SQ SEQUENCE 653 AA; 72701 MW; 5875B4E9C2F4FC82 CRC64;

Query Match 73.3%; Score 33; DB 1; Length 653;
 Best Local Similarity 75.0%; Pred. No. 61;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLHDDLE 8
 :|||||
 Db 72 ILHDDLE 79

RESULT 12
 RII5_YEAST
 ID RII5_YEAST STANDARD; PRT; 1770 AA.
 AC P43565;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE SERINE/THREONINE-PROTEIN KINASE RIM15 (EC 2.7.1.-).
 GN RIM15 OR TAK1 OR YFL033C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 [1]
 SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
 RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
 RA Yamazaki M., Tashiro H., Eki T.;
 RT "Analysis of the nucleotide sequence of chromosome VI from
 RT Saccharomyces cerevisiae.";
 RL Nac. Genet. 10:261-268(1995).
 [2]
 SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC MEDLINE=97265402; PubMed=9111339;
 RA Vidan S., Mitchell A.P.;
 RT "Stimulation of yeast meiotic gene expression by the
 RT glucose-repressible protein kinase Rim15p.";
 RL Mol. Cell. Biol. 17:2688-2697(1997).
 [3]
 SEQUENCE FROM N.A.
 RA Reinders A., Buerkert N., Boller T., Wienken A., de Virgilio C.;
 RT "Saccharomyces cerevisiae cAMP-dependent protein kinase controls entry
 RT into stationary phase through the Rim15p protein kinase.";
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: INVOLVED IN THE ACTIVATION OF A MEIOTIC GENES ACTIVATION
 CC PATHWAY.

CC -1- PTM: AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
 CC PROTEIN KINASES. STRONG, WITH S.POMBE CEK1.

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CC EMBL; D50617; BAA09206.1; -.
 DR EMBL; U83459; AAB64088.1; -.
 DR EMBL; AJ001030; CAA04486.1; -.
 DR HSP; Q63450; 1A06.
 DR SGD; S0001861; RIM15.
 DR InterPro; IPR000719; -.
 DR InterPro; IPR001789; -.

DR InterPro: IPR002290; 2.
 DR Pfam: PF00069; kinase; 2.
 DR Pfam: PF00072; response_reg; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR Transferrase: Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation; Melosis.
 FT DOMAIN 343 358 POLY-ASN.
 FT DOMAIN 620 624 POLY-SER.
 FT NP_BIND 800 808 PROTEIN KINASE.
 FT BINDING 823 823 ATP (BY SIMILARITY).
 FT ACT_SITE 918 918 BY SIMILARITY.
 FT DOMAIN 975 980 POLY-ASN.
 FT DOMAIN 1213 1218 POLY-GLU.
 FT DOMAIN 1386 1391 POLY-THR.
 SQ SEQUENCE 1770 AA; 196530 MW; DC1064825000FAFF CRC64;

Query Match 73.3%; Score 33; DB 1; Length 1770;
 Best Local Similarity 75.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDLE 8

Db 272 LLDHMLE 279

RESULT 13
 ID RLAL_CHLRE STANDARD; PRT; 107 AA.
 AC P29763;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE 60S ACIDIC RIBOSOMAL PROTEIN P1.
 OS Chlamydomonas reinhardtii.
 CC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 CC Chlamydomonadaceae; Chlamydomonas.
 OX NCBI_TaxID=3055;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=137C;
 RA Dumont F.;
 RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE ELONGATION STEP OF
 CC PROTEIN SYNTHESIS (BY SIMILARITY).
 CC -!- SUBUNIT: P1 AND P2 EXIST AS DIMERS AT THE LARGE RIBOSOMAL
 CC SUBUNIT (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.

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 or send an email to license@isb-sib.ch).

DR EMBL: X66411; CAA47042.1; .
 DR PIR: S24990; R6KWL;
 DR InterPro: IPR001813; .
 DR Pfam: PF00428; 60s_Ribosomal; 1.
 KW Ribosomal protein.
 SQ SEQUENCE 107 AA; 10875 MW; 2A7FC9696D8617EF CRC64;

Query Match 71.1%; Score 32; DB 1; Length 107;
 Best Local Similarity 75.0%; Pred. No. 12;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLE 8

Db 14 ILHDDGLE 21

RESULT 14
 ID YVAE_VACCC STANDARD; PRT; 166 AA.
 AC P20514;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE HYPOTHETICAL 18.2 KDA PROTEIN.
 GN A ORF E.
 OS Vaccinia virus (strain Copenhagen).
 CC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 CC Orthopoxvirus.
 OX NCBI_TaxID=10249;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91021027; PubMed=2219722;
 RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
 RA Paoletti E.;
 RT "The complete DNA sequence of vaccinia virus.";
 RL Virology 179:247-266(1990).

CC COMPLETE GENOME.
 RN [2]
 RP GOEBEL S.J., JOHNSON G.P., PERKUS M.E., DAVIS S.W., WINSLOW J.P.,
 RA Paoletti E.;
 RL Virology 179:517-563(1990).
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DR EMBL: M35027; AAA48130.1; .
 DR PIR: A42524; A42524.
 KW Hypothetical protein.
 SQ SEQUENCE 166 AA; 18230 MW; 5927A96A0CB9477B CRC64;

Query Match 71.1%; Score 32; DB 1; Length 166;
 Best Local Similarity 55.6%; Pred. No. 20;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLEA 9

Db 12 ILHDDCLKS 20

RESULT 15
 ID BZLF_EBV STANDARD; PRT; 245 AA.
 AC P03206;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE BZLF1 TRANS-ACTIVATOR PROTEIN (EB1) (ZEBRA).
 GN BZLF1.
 OS Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
 CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 CC Gammaherpesvirinae; Lymphocryptovirus.
 OX NCBI_TaxID=10377;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84270667; PubMed=6087149;
 RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
 RA Gibson T.J., Hatfull G., Hudson G.S., Sachwell S.C., Seguin C.,
 RA Tuffnell P.S., Barrett B.G.;
 RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";

```

RL Nature 310:207-211(1984).
RN [2]
RP IDENTIFICATION OF PROTEIN.
RX MEDLINE-87311873; PubMed-3041034;
RA Biggin M., Bodescot M., Perricaudet M., Farrel P.;
RT "Epstein-Barr virus gene expression in P3HR1-superinfected Raji
RL cells.";
RL J. Virol. 61:3120-3132(1987).
RN [3]
RP DNA-BINDING.
RX MEDLINE-89231610; PubMed-2540954;
RA Farrel P.J., Rowe D.T., Rooney C.M., Kouzarides T.;
RT "Epstein-Barr virus BzLF1 trans-activator specifically binds to a
RL consensus AP-1 site and is related to c-fos.";
RL EMBO J. 8:127-132(1989).
RN [4]
RP STRUCTURE, AND FUNCTION.
RX MEDLINE-90219210; PubMed-2157874;
RA Packham G., Economou A., Rooney C.M., Rowe D.T., Farrel P.J.;
RT "Structure and function of the Epstein-Barr virus BZLF1 protein.";
RL J. Virol. 64:2110-2116(1990).
RN [5]
RP FUNCTION.
RX MEDLINE-94008999; PubMed-8404860;
RA Schepers A., Pich D., Hamerschmidt W.;
RT "A transcription factor with homology to the AP-1 family links RNA
RL transcription and DNA replication in the lytic cycle of Epstein-Barr
RL virus.";
RL EMBO J. 12:3921-3929(1993).
CC -1- FUNCTION: BZLF1 PLAYS A KEY ROLE IN THE SWITCH FROM LATENT TO
CC PRODUCTIVE INFECTION OF EBV. BZLF1 ACTIVATES THE PROMOTER OF AN
CC OTHER EBV GENE (BSLF2+BMFL1).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: TO OTHER BZIP PROTEINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: V01555; CAA24861.1; -
DR PIR: A03768; QBE27.
DR PIR: S03634; S03634.
DR TRANSFAC: T00923; -
DR InterPro: IPR001871; -
DR Pfam: PF00170; bZIP; 1.
DR PROSITE: PS00036; BZIP_BASIC; 1.
KW Transcription regulation; DNA-binding; Nuclear protein; Early protein.
FT DNA_BIND 178 195 BASIC MOTIF
SQ SEQUENCE 245 AA; 26860 MW; 7F3D55D79F1F0196 CRC64;

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Query Match 71.1%; Score 32; DB 1; Length 245;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLHDDLL 7
Db 237 VLHEDLL 243

```

Search completed: July 10, 2001, 08:35:27
Job time: 250 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 10, 2001, 08:31:47 ; Search time 33.27 Seconds
(without alignments)
35.790 Million cell updates/sec

Title: US-09-489-760-2

Perfect score: 45

Sequence: 1 VLHDDLLLEA 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL16.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_unclassified.*
13: sp_vertebrate.*
14: sp_virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	84.4	1148	3 Q03897	Q03897 saccharomyc
2	37	82.2	1165	4 Q92619	Q92619 homo sapien
3	35	77.8	119	9 Q80057	Q80057 bacterioph
4	35	77.8	496	9 Q8MBP0	Q8MBP0 staphylococ
5	35	77.8	616	1 Q27025	Q27025 methanobact
6	34	75.6	332	5 Q9V966	Q9V966 drosophila
7	34	75.6	640	5 Q9NKM2	Q9NKM2 leishmania
8	34	75.6	741	5 Q25257	Q25257 leishmania
9	34	75.6	741	5 Q9NDK7	Q9NDK7 leishmania
10	34	75.6	774	5 Q9VA13	Q9VA13 drosophila
11	34	75.6	1383	5 Q9VDA0	Q9VDA0 drosophila
12	33	73.3	145	2 Q93387	Q93387 staphylococ
13	33	73.3	174	5 Q94256	Q94256 caenorhabdi
14	33	73.3	175	2 Q9RPT9	Q9RPT9 streptomyce
15	33	73.3	210	2 Q9S3K5	Q9S3K5 staphylococ
16	33	73.3	238	2 P74656	P74656 synecocyst
17	33	73.3	247	2 Q9SOL4	Q9SOL4 staphylococ
18	33	73.3	259	2 Q9PBQ0	Q9PBQ0 xylella fas
19	33	73.3	291	2 Q911R8	Q911R8 pseudomonas

20	33	73.3	319	14 Q9WHJ4	Q9WHJ4 walleye epi
21	33	73.3	320	2 Q9RVU0	Q9RVU0 deinococcus
22	33	73.3	322	2 Q9HVL5	Q9HVL5 pseudomonas
23	33	73.3	352	2 Q9RJH5	Q9RJH5 streptomyce
24	33	73.3	378	2 Q9X7V8	Q9X7V8 streptomyce
25	33	73.3	398	1 Q9YE58	Q9YE58 aeropyrum p
26	33	73.3	408	5 Q9V8W8	Q9V8W8 drosophila
27	33	73.3	416	10 Q9FWD0	Q9FWD0 oryza sativ
28	33	73.3	421	1 P94942	P94942 methanopyru
29	33	73.3	425	6 Q9GM45	Q9GM45 macaca fasc
30	33	73.3	654	2 Q9LAM6	Q9LAM6 salmonella
31	33	73.3	723	10 Q9SV54	Q9SV54 arabidopsis
32	33	73.3	856	10 Q9SV11	Q9SV11 arabidopsis
33	33	73.3	908	2 Q87123	Q87123 vibrio algi
34	33	73.3	973	3 Q9UR24	Q9UR24 schizosacch
35	33	73.3	1534	4 Q9UF04	Q9UF04 homo sapien
36	33	73.3	4150	2 Q9KIV4	Q9KIV4 streptomyce
37	32	71.1	91	2 Q07938	Q07938 bacillus su
38	32	71.1	166	14 Q9JF89	Q9JF89 vaccinia vi
39	32	71.1	240	11 Q63432	Q63432 rattus norv
40	32	71.1	245	14 Q69127	Q69127 human herpe
41	32	71.1	253	5 Q9N3G0	Q9N3G0 caenorhabdi
42	32	71.1	270	1 Q9H8H9	Q9H8H9 halobacteri
43	32	71.1	276	5 Q44591	Q44591 caenorhabdi
44	32	71.1	282	1 Q9FNI3	Q9FNI3 arabidopsis
45	32	71.1	294	1 Q54288	Q54288 sulfolobus

ALIGNMENTS

RESULT 1

Q03897 ID Q03897 PRELIMINARY; PRT; 1148 AA.
AC Q03897;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE HYPOTHEtical 130.9 KDA PROTEIN.
GN YDRL28W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB972;
RA Oliver K., Harris D.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB972;
RA Barrell B., Rajandream M.A.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z48179; CA88209.1; -
DR SGB; S0002535; YDRL28W.
DR InterPro; IPR001680; -
DR Pfam; PF00400; WD40; 6.
DR PRINTS; PR00320; GPROTEINRPT.
DR PROSITE; PS00678; WD_REPEATS; UNKNOWN_1.
DR SMART; SM00320; WD40; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 1148 AA; 130945 MW; D6A137FB0FDE2816 CRC64;

Query Match 84.4%; Score 38; DB 3; Length 1148;
Best Local Similarity 66.7%; Pred. No. 86;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDLLLEA 9

:|||||:

Db 1001 LLHDDIIIEA 1009


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RESULT 2
Q92619 ID Q92619 PRELIMINARY; PRT; 1165 AA.
AC Q92619
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE MYELOBLAST KIAA0223 (FRAGMENT).
GN KIAA0223.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RX MEDLINE=97191544; PubMed=9039502;
RA Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayashi Y., Ohara O.,
RA Tanaka A., Kotani H., Miyajima N., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. VI.
RT The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
RT analysis of cDNA clones from cell line KG-1 and brain.";
RL DNA Res. 3:321-329(1996).
RN [2]
RP SEQUENCE OF 170-1165 FROM N.A.
RA Lanerding J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
RA Phan H., Velasco N., Ganes J., Danganan L., Poundstone P.,
RA Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T.,
RA Trankheim M., Amico-Keller G., Coffield J., Duarte S., Lucas S.,
RA Bruce R., Thomas P., Quan G., Knecht Miller B., Arellano A.,
RA Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,
RA Carrano A.V.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; D86976; BAAL3121.1; -.
DR EMBL; AC004151; AAC03237.1; -.
DR HSSP; Q07960; IRGP.
DR InterPro; IPR000198; -.
DR InterPro; IPR002219; -.
DR Pfam; PF00130; DAG_PE_bind; 1.
DR Pfam; PF00620; RhogAP; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; UNKNOWN_1.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR SMART; SM00324; RhogAP; 1.
FT NON_TER
FT 1
SQ SEQUENCE 1165 AA; 127344 MW; 92EF769CAFD458C9 CRC64;

Query Match 82.2%; Score 37; DB 4; Length 1165;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLLA 9
Db 166 VLRDDLLA 174

RESULT 3
O80057 ID O80057 PRELIMINARY; PRT; 119 AA.
AC O80057
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE ORF 18.
OS bacteriophage phi PVL.
OC Viruses.
OX NCBI_TaxID=71366;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98067870; PubMed=9404084;
RA Kaneko J., Kimura T., Kawakami Y., Tomita T., Kamio Y.;

Query Match 82.2%; Score 37; DB 4; Length 1165;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLLA 9
Db 166 VLRDDLLA 174

RESULT 5
O27025 ID O27025 PRELIMINARY; PRT; 616 AA.
AC O27025
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE TYPE I RESTRICTION MODIFICATION ENZYME, SUBUNIT M.
GN MTH942.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanothermobacter.
OX NCBI_TaxID=145262;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DELTA H;
RX MEDLINE=98037514; PubMed=9371463;

Query Match 77.8%; Score 35; DB 9; Length 496;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HDDLLEA 9
Db 72 HDDLLEA 78

RESULT 5
O27025 ID O27025 PRELIMINARY; PRT; 616 AA.
AC O27025
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE TYPE I RESTRICTION MODIFICATION ENZYME, SUBUNIT M.
GN MTH942.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanothermobacter.
OX NCBI_TaxID=145262;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DELTA H;
RX MEDLINE=98037514; PubMed=9371463;

Query Match 77.8%; Score 35; DB 9; Length 496;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HDDLLEA 9
Db 72 HDDLLEA 78

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RT "Panton-valentine leukocidin genes in a phage-like particle isolated
RT from mitomycin C-treated Staphylococcus aureus V8 (ATCC 49775).";
RL Biosci. Biotechnol. Biochem. 61:1960-1962(1997).
SQ SEQUENCE 119 AA; 13921 MW; 0F2A472DB7D63FA0 CRC64;

Query Match 77.8%; Score 35; DB 9; Length 119;
Best Local Similarity 85.7%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HDDLLEA 9
Db 72 HDDLLEA 78

RESULT 4
Q9MBP0 ID Q9MBP0 PRELIMINARY; PRT; 496 AA.
AC Q9MBP0
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE PHI PVL ORF 18 AND 19 HOMOLOGUE.
OS Staphylococcus aureus prophage phiPv83.
OC Viruses.
OX NCBI_TaxID=129009;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P83;
RA Zou D., Kaneko J., Narita S., Kamio Y.;
RT "Complete nucleotide sequence and molecular characterization of
RT prophage pV83pro carrying lukM-lukP-PV(p83) gene cluster in
RT Staphylococcus aureus strain P83.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=P83;
RX MEDLINE=98067870; PubMed=9404084;
RA Kaneko J., Muramoto K., Kamio Y.;
RT "Gene of LukF-PV-like component of Panton-Valentine leukocidin in
RT Staphylococcus aureus p83 is linked with lukM";
RL Biosci. Biotechnol. Biochem. 61:1960-1962(1997).
DR EMBL; AB044554; BAA97859.1; -.
SQ SEQUENCE 496 AA; 56878 MW; 1BE4F6E6D7920584 CRC64;

Query Match 77.8%; Score 35; DB 9; Length 496;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HDDLLEA 9
Db 72 HDDLLEA 78

```


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OM protein - protein search, using sw model

Run on: July 10, 2001, 08:35:27 ; Search time 12.64 Seconds
(without alignments)
24.391 Million cell updates/sec

Title: US-09-489-760-5

Perfect score: 42

Sequence: 1 VLKDDLEA 9

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	34	81.0	282	1 FU34_YEAST	P32907 saccharomyc
2	34	81.0	343	1 G3P_METJA	Q58546 methanococ
3	34	81.0	3519	1 OL56_STRAT	Q07017 streptomyce
4	33	78.6	465	1 RBL_DAPSP	P28397 daphniphyll
5	33	78.6	822	1 EPS8_HUMAN	Q12929 homo sapien
6	33	78.6	1041	1 SY1_MYCTU	Q10765 mycobacteri
7	33	78.6	1059	1 SY1_MYCLE	Q9x7e5 mycobacteri
8	32	76.2	264	1 YCV5_SCHPO	Q13679 schizosacch
9	32	76.2	334	1 NA37_ECOLI	P33920 escherichia
10	32	76.2	372	1 YC60_MYCTU	Q11058 mycobacteri
11	32	76.2	447	1 RBL_CONTR	Q05988 convolvulus
12	32	76.2	465	1 RBL_PLAOC	P28441 platanus oc
13	32	76.2	465	1 RBL_PROAR	P28458 trochodendr
14	32	76.2	499	1 AMPA_CHLPN	Q928f8 chlamydia p
15	32	76.2	598	1 CYSJ_ECOLI	P38038 escherichia
16	32	76.2	598	1 CYSJ_SALTY	P38039 salmonella
17	32	76.2	889	1 NTA3_MAIZE	P49102 zea mays (m
18	31	73.8	112	1 GUNB_RHOSH	P43519 rhodobacter
19	31	73.8	252	1 VMT1_IABAN	P03487 influenza a
20	31	73.8	252	1 VMT1_IACKB	P36347 influenza a
21	31	73.8	252	1 VMT1_IACOW	P10918 influenza a
22	31	73.8	252	1 VMT1_IAPFR	P03488 influenza a
23	31	73.8	252	1 VMT1_IAPFW	P05775 influenza a
24	31	73.8	252	1 VMT1_IAMAN	P08381 influenza a
25	31	73.8	252	1 VMT1_IAUDO	P03486 influenza a
26	31	73.8	252	1 VMT1_IJAVI	P05777 influenza a
27	31	73.8	252	1 VMT1_IJAZ1	P05776 influenza a
28	31	73.8	441	1 RBL_FOUPSP	Q05990 fouquieria
29	31	73.8	508	1 Y020_HUMAN	Q15397 homo sapien
30	31	73.8	593	1 GDR1_SCHPO	P07334 schizosacch
31	31	73.8	629	1 HAPI_RAT	P54256 rattus norv
32	31	73.8	682	1 RECG_BACSU	Q34942 bacillus su
33	31	73.8	862	1 GYRA_CAMFE	P47235 campylobact

34 31 73.8 921 1 SY1_BACSU
35 31 73.8 1128 1 BEM3_YEAST
36 31 73.8 1300 1 DYM3_NEUCR
37 31 73.8 2504 1 PAS_HUMAN
38 31 73.8 3149 1 TEGU_EBV
39 30 71.4 195 1 NIFQ_AZOVI
40 30 71.4 231 1 YHHW_ECOLI
41 30 71.4 267 1 EUTT_ECOLI
42 30 71.4 267 1 EUTT_SALTY
43 30 71.4 338 1 CYF_PHOLA
44 30 71.4 368 1 SERC_NEIMA
45 30 71.4 368 1 SERC_NEIMB

ALIGNMENTS

RESULT 1
FU34_YEAST
ID FU34_YEAST STANDARD; PRT; 282 AA.
AC P32907;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE FUN34 PROTEIN.
GN FUN34 OR YNR002C OR N2029.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GRF88;
RX MEDLINE=93016077; PubMed=1400451;
RA Stettler S., Mariotte S., Riva M., Sentenac A., Thuriaux P.;
RT "An essential and specific subunit of RNA polymerase III (C) is
RT encoded by gene RPC34 in Saccharomyces cerevisiae.";
RL J. Biol. Chem. 267:21390-21395(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GRF88;
RX MEDLINE=95028151; PubMed=7941739;
RA Lalo D., Stettler S., Mariotte S., Gendreau E., Thuriaux P.;
RT "Organization of the centromeric region of chromosome XIV in
RT Saccharomyces cerevisiae.";
RL Yeast 10:523-533(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1679;
RX MEDLINE=95208356; PubMed=7500425;
RA Verhasselt P., Aert R., Voet M., Voickaert G.;
RT "Twelve open reading frames revealed in the 23.6 kb segment flanking
RT the centromere on the Saccharomyces cerevisiae chromosome XIV right
RL arm.";
RL Yeast 10:1355-1361(1994).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE GPRL/FUN34/YAAH FAMILY.
CC
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CC
CC EMBL: X63746; CAA5279.1; -
CC EMBL: X77395; CAA54571.1; -
CC EMBL: Z71617; CAA96278.1; -
CC PIR: S31258; S31258.
CC SGD: S0005285; FUN34.
CC InterPro: IPR000791; -
CC Pfam: PF01184; Gppl_Fun34_Yeah; 1.

DR PROSITE; PS01114; GPR1_FUN34_YAAH; 1.
KW Transmembrane.
FT TRANSMEM 87 107 POTENTIAL.
FT TRANSMEM 120 140 POTENTIAL.
FT TRANSMEM 151 171 POTENTIAL.
FT TRANSMEM 185 205 POTENTIAL.
FT TRANSMEM 208 228 POTENTIAL.
FT TRANSMEM 239 259 POTENTIAL.
SQ SEQUENCE 282 AA; 30701 MW; F5E20F9324CE8199 CRC64;

Query Match 81.0%; Score 34; DB 1; Length 282;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Caps 0;

OY 2 LRDLLEA 9
| | | | |
DB 62 LRDLLEA 59

RESULT 2
G3P_METJA STANDARD; PRT; 343 AA.
AC Q58546;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 38, Last annotation update)
DE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12) (GAPDH).
GN GAP OR Mcl146.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
ON NCBI_TaxID=21190;
RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Sult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii";
RL Science 273:1058-1073(1996).

CC -!- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE
CC + NAD(+) = 1,3-DIPHOSPHATEGLYCERATE + NADH.
CC -!- PATHWAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.
CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
CC DEHYDROGENASE FAMILY.
CC
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CC
CC EMBL; U67557; AB99147.1; -
CC TIGR; M1446; -
CC InterPro; IPR000173; -
CC Pfam; PF00044; gpdh; 1.
CC PROSITE; PS00071; GAPDH; 1.
CC GLYCOLYSIS; Oxidoreductase; NAD; NADP.
CC BINDING 144 144
CC SIMILARITY: GLYCERALDEHYDE 3-PHOSPHATE (BY
CC SIMILARITY).
CC SEQUENCE 343 AA; 38102 MW; 81EB5810A9C838C5 CRC64;

Query Match 81.0%; Score 34; DB 1; Length 343;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Caps 0;

OY 1 VLRDDLEA 9
| | | | |
DB 238 VSRDDLEA 246

RESULT 3
OL56_STRAT STANDARD; PRT; 3519 AA.
AC Q07017;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE OLEANDOMYCIN POLYKETIDE SYNTHASE, MODULES 5 AND 6.
GN ORFB.
OS Streptomyces antibioticus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1890;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150470; PubMed=8107583;
RA Swan D.G., Rodriguez A.M., Vilches C., Mendez C., Salas J.A.;
RT "Characterisation of a Streptomyces antibioticus gene encoding a type
I polyketide synthase which has an unusual coding sequence.";
RL Mol. Gen. Genet. 242:358-362(1994).
CC -!- FUNCTION: MAY BE INVOLVED IN THE BIOSYNTHESIS OF THE OLEANDOMYCIN
CC LACTONE RING.
CC -!- COFACTOR: CONTAINS 1 COVALENTLY BOUND PHOSPHOPANTETHEINE.
CC -!- SIMILARITY: TO FATTY ACID SYNTHASE (FAS).
CC

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CC
CC EMBL; L09654; AA19695.1; -
CC HSSP; P25715; IMLA.
CC InterPro; IPR000255; -
CC InterPro; IPR000794; -
CC InterPro; IPR001031; -
CC InterPro; IPR001227; -
CC Pfam; PF00698; Acyl_transf; 2.
CC Pfam; PF00975; Thioesterase; 1.
CC Pfam; PF00109; ketoacyl-synt; 2.
CC Pfam; PF00550; pp-binding; 2.
CC PROSITE; PS00012; PHOSPHOPANTETHEINE; 2.
CC PROSITE; PS00606; B-KETOACYL-SYNTHASE; 2.
CC PROSITE; PS00075; ACP_DOMAIN; 2.
CC Transferrase; Acyltransferase; Antibiotic biosynthesis; NADP;
KW Phosphopantetheine; Multifunctional enzyme.
FT DOMAIN 1 ? MODULE 5.
FT DOMAIN ? 3519 MODULE 6.
FT DOMAIN 32 501 BETA-KETOACYL SYNTHASE (KS).
FT DOMAIN 569 890 ACYLTRANSFERASE (AT).
FT DOMAIN 1200 1362 BETA-KETOACYL REDUCTASE (KR).
FT DOMAIN 1487 1561 ACYL CARRIER (ACP).
FT DOMAIN 1686 2156 BETA-KETOACYL SYNTHASE (KS).
FT DOMAIN 2220 2541 ACYLTRANSFERASE (AT).
FT DOMAIN 2856 3038 BETA-KETOACYL REDUCTASE (KR).
FT DOMAIN 3141 3215 ACYL CARRIER (ACP).
FT ACT_SITE ? ? ACYL-ENZYME INTERMEDIATE.
FT BINDING ? ? PHOSPHOPANTETHEINE (BY SIMILARITY).
FT BINDING 3270 3519 THIOESTERASE.
FT ACT_SITE 210 210 BETA-KETOACYL SYNTHASE.

FT ACT_SITE 660 660 ACYL-ENZYME INTERMEDIATE.
 FT NP_BIND 1203 1249 NADP.
 FT BINDING 1524 1524 PHOSPHOPANTETHEINE (BY SIMILARITY).
 FT ACT_SITE 1859 1859 BETA-KETOACYL SYNTHASE.
 FT ACT_SITE 2311 2311 ACYL-ENZYME INTERMEDIATE.
 FT NP_BIND 2859 2905 NADP.
 FT BINDING 3178 3178 PHOSPHOPANTETHEINE (BY SIMILARITY).
 SQ SEQUENCE 3519 AA; 368561 MW; 41AE78AAAE61F86 CRC64;

Query Match 81.0%; Score 34; DB 1; Length 3519;
 Best Local Similarity 87.5%; Pred. No. 1.9e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLEA 9
 DB 770 LRDELLEA 777

RESULT 4
 ID RBL_DAPSP STANDARD; PRT; 465 AA.
 AC P28397;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO
 DE LARGE SUBUNIT) (FRAGMENT).
 GN RBCL.
 OS Chloroplast.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Saxifragales;
 OC Daphniphyllaceae; Daphniphyllum.
 OX NCBI_TaxID=4388;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92397008; PubMed=1523408;
 RA Albert V.A., Williams S.E., Chase M.W.;
 RT "Carnivorous plants: phylogeny and structural evolution.";
 RL Science 257:1491-1495(1992);
 CC -!- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF
 CC D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC
 CC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF
 CC THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
 CC REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
 CC ACTIVE SITE.
 CC -!- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) =
 CC 2 3-PHOSPHO-D-GLYCERATE.
 CC -!- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) =
 CC 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
 CC -!- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -!- SIMILARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; L01901; AAA84198.2; -
 CC DR HSSP; P00875; LRPX.
 CC DR Mendel; 5117; DAPsp; rbcL; 1.
 CC DR InterPro; IPR000685; -
 CC DR Pfam; PF00016; RUBISCO_large; 1.
 CC DR PROSITE; PS00157; RUBISCO_LARGE; 1.
 KW Photosynthesis; Carbon dioxide fixation; Photorespiration;
 KW Lyase; Oxidoreductase; Monooxygenase; Chloroplast.
 FT NON_TER 1 1
 FT ACT_SITE 191 191 BINDING OF CO(2) ACTIVATES THE ENZYME.

SQ SEQUENCE 465 AA; 51606 MW; 019A80B3B25957EF CRC64;

Query Match 78.6%; Score 33; DB 1; Length 465;
 Best Local Similarity 75.0%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLRODLE 8
 DB 338 LRDDLE 345

RESULT 5
 ID EPS8_HUMAN STANDARD; PRT; 822 AA.
 AC Q12929;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.
 GN EPS8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94366756; PubMed=8084614;
 RA Wong W.T., Carlomagno F., Druck T., Barletta C., Croce C.M.,
 RA Huebner K., Kraus M.H., di Fiore P.P.;
 RT "Evolutionary conservation of the EPS8 gene and its mapping to human
 RT chromosome 1q23-q24.".
 RL Oncogene 9:3057-3061(1994).
 CC -!- FUNCTION: UPON BINDING TO EGF RECEPTOR ENHANCES EGF-DEPENDENT
 CC MITOGENIC SIGNALS. CAN BIND MULTIPLE CELLULAR TARGETS.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES ANALYZED, INCLUDING
 CC HEART, BRAIN, PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY AND
 CC PANCREAS. EXPRESSED IN ALL EPITHELIAL AND FIBROBLASTIC LINES
 CC EXAMINED AND IN SOME, BUT NOT ALL, HEMATOPOIETIC CELLS.
 CC -!- PTM: PHOSPHORYLATED BY SEVERAL RECEPTOR TYROSINE KINASES.
 CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 SPLIT PH DOMAIN.
 CC -----
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 CC -----
 CC EMBL; U12535; AAA62280.1; -
 CC DR HSSP; Q08509; 1A0J.
 CC DR MIM; 600206; -
 CC DR InterPro; IPR001452; -
 CC DR Pfam; PF00018; SH3; 1.
 CC DR PROSITE; PS50002; SH3; 1.
 CC KW SH3 domain; Phosphorylation.
 CC FT DOMAIN 69 129 PH (FIRST PART).
 CC FT DOMAIN 210 213 POLY-PRO.
 CC FT DOMAIN 322 325 POLY-PRO.
 CC FT DOMAIN 381 414 PH (SECOND PART).
 CC FT DOMAIN 421 440 PRO-RICH.
 CC FT DOMAIN 532 591 SH3.
 CC FT DOMAIN 615 651 PRO-RICH.
 CC FT DOMAIN 659 664 POLY-SER.
 CC FT SEQUENCE 822 AA; 91881 MW; AC5EB1D28B784B3B CRC64;

Query Match 78.6%; Score 33; DB 1; Length 822;
 Best Local Similarity 75.0%; Pred. No. 60;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLRDLDLE 8
DB 552 VLKDDILE 559

RESULT 6

SYL_MYCTU STANDARD; PRT: 1041 AA.
AC Q10765; 006181;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE)
DE (ILERS).
GN ILES OR RV1536 OR MTCY48.29C.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaita F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E.,
RA Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).

CC -1- CATALYTIC ACTIVITY: ATP + L-ISOLEUCINE + TRNA(ILE) = AMP +
CC PYROPHOSPHATE + L-ISOLEUCYL-TRNA(ILE).
CC -1- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC
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CC
CC EMBL: Z74020; CA98326.1; -;
CC TubercuList; RV1536; -;
CC InterPro: IPR001412; -;
CC InterPro: IPR002300; -;
CC Pfam: PF00133; trna-synt_1; 1.
CC PRINTS: PR00984; TRNASYNTHILE.
CC PROSITE: PS00178; AA_TRNA_LIGASE_I; 1.
CC Aminoacyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC Metal-binding; Zinc.
CC SITE 53 63 "HIGH" REGION.
CC SITE 619 623 "KMSKS" REGION.
CC BINDING 622 622 ATP (BY SIMILARITY).
CC SEQUENCE 1041 AA; 117339 MW; B5023822848E08C6 CRC64;

Query Match 78.6%; Score 33; DB 1; Length 1041;
Best Local Similarity 77.8%; Pred. No. 78;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLRDLDLE 9
DB 710 VLKDDLES 718

RESULT 7

SYL_MYCLE STANDARD; PRT: 1059 AA.
AC Q9X7E5;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE)
DE (ILERS).
GN ILES OR MLCB458.10.
OS Mycobacterium leprae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Seeger K.J., Harris D., James K.D., Parkhill J., Barrell B.G.,
RA Rajandream M.A.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + L-ISOLEUCINE + TRNA(ILE) = AMP +
CC PYROPHOSPHATE + L-ISOLEUCYL-TRNA(ILE).
CC -1- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC
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CC
CC EMBL: AL049478; CAB39575.1; -;
CC InterPro: IPR002300; -;
CC InterPro: IPR002301; -;
CC Pfam: PF00133; trna-synt_1; 1.
CC PRINTS: PR00984; TRNASYNTHILE.
CC PROSITE: PS00178; AA_TRNA_LIGASE_I; 1.
CC Aminoacyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC Metal-binding; Zinc.
CC SITE 59 69 "HIGH" REGION.
CC SITE 637 641 "KMSKS" REGION.
CC BINDING 640 640 ATP (BY SIMILARITY).
CC SEQUENCE 1059 AA; 119808 MW; 67FC7659E9399E39 CRC64;

Query Match 78.6%; Score 33; DB 1; Length 1059;
Best Local Similarity 77.8%; Pred. No. 79;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLRDLDLE 9
DB 728 VLKDDLSQA 736

RESULT 8

YCV5_SCHPO STANDARD; PRT: 264 AA.
AC O13679;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 30.7 KDA PROTEIN C737.05 IN CHROMOSOME III.
DE SPCC737.05.
GN Schizosaccharomyces pombe (Fission yeast).
OS Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;

RA Murphy L., Harris D., Wood V., Lyne M.H., Rajandream M.A.,
 RA Barrell B.G.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC
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 CC
 DR EMBL: AL031546; CAB44773.1; -
 DR EMBL: AL031546; CAB44773.1; -
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 48 68 POTENTIAL.
 FT TRANSMEM 112 132 POTENTIAL.
 FT TRANSMEM 142 162 POTENTIAL.
 SQ SEQUENCE 264 AA; 30665 MW; D0EE75C409F09F0B CRC64;

Query Match 76.2%; Score 32; DB 1; Length 264;
 Best Local Similarity 55.6%; Pred. No. 27;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLRDILLEA 9
 : : : : :
 DB 26 IIRDELVEA 34

RESULT 9
 NA37_ECOLI STANDARD; PRT; 334 AA.
 AC P33920;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 37 KDA NUCLEOID-ASSOCIATED PROTEIN.
 GN YEJ3.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia
 OC NCBI_TaxID=562;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / BHB2600;
 RA Richterich P., Lakey N., Gryan G., Jaehn L., Mintz L., Robison K.,
 RA Church G.M.;
 RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12."
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE OF 1-15.
 RX MEDLINE=99296598; PubMed=10368163;
 RA Murphy L.D., Rosner J.L., Zimmerman S.B., Esposito D.;
 RT "Identification of two new proteins in spermidine nucleoids isolated
 from Escherichia coli."
 RL J. Bacteriol. 181:3842-3844(1999).
 CC -|- FUNCTION: NOT KNOWN
 CC -|- SUBCELLULAR LOCATION: SEEMS TO BE ASSOCIATED WITH THE NUCLEOID.
 CC -|- SIMILARITY: STRONG, TO H. INFLUENZAE HI0839.

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 CC

DR EMBL: U00008; AAA16382.1; -
 DR EMBL: AE000308; AAC75247.1; -
 DR EcoGene: EG12048; yejK.
 FT INIT_MET 0
 SQ SEQUENCE 334 AA; 37691 MW; 9BBB724479F8E335 CRC64;

Query Match 76.2%; Score 32; DB 1; Length 334;
 Best Local Similarity 87.5%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLRDILLE 8
 : : : : :
 DB 23 VLRDILLE 30

RESULT 10
 YC60_MYCTU STANDARD; PRT; 372 AA.
 ID YC60_MYCTU
 AC Q11058;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE HYPOTHETICAL 41.3 KDA PROTEIN RV1260.
 GN RV1260 OR MTCV50.22C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OC NCBI_TaxID=1773;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Horsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E.,
 RA Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 complete genome sequence."
 RL Nature 393:537-544(1998).

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 CC

DR EMBL: 277137; CAB00893.1; -
 DR Tuberculin; RV1260;
 DR InterPro: IPR000733; -
 DR InterPro: IPR002938; -
 DR Pfam: PF01494; FAD_binding_3; 1.
 DR Pfam: PF01360; Monooxygenase; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 372 AA; 41329 MW; C2E5BE08D68E29FF CRC64;

Query Match 76.2%; Score 32; DB 1; Length 372;
 Best Local Similarity 75.0%; Pred. No. 40;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLRDILLE 8

Db 102 LLRDDLVE 109
:|||||:

RESULT 11

RBL_CONTR
ID RBL_CONTR STANDARD; PRT; 447 AA.
AC Q05988;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RUBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO
DE LARGE SUBUNIT) (FRAGMENT).
DE RBL.
GN NCBL_TaxID=4124;
OS Convolvulus tricolor.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Solanales; Convolvulaceae; Convolvulus.
OX NCBL_TaxID=4124;
RN [1]
SEQUENCE FROM N.A.
RA Olmstead R.G., Michaels H.J., Scott K.M., Palmer J.D.;
RT "Monophyly of the Asteridae and identification of their major lineages
RT inferred from DNA sequences of rbcL";
RL Ann. Mo. Bot. Gard. 79:249-265(1992).
CC -!- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF
CC D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC
CC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF
CC THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
CC REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
CC ACTIVE SITE.
CC -!- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) =
CC 2 3-PHOSPHO-D-GLYCERATE.
CC -!- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) =
CC 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
CC -!- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- SIMILARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.
CC
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CC
CC EMBL; L11693; AAA84131.1; -
CC HSP; P00876; 3RUB.
CC InterPro: IPR000685; -
CC Pfam: PF00016; RUBISCO_large; 1.
CC PROSITE: PS00157; RUBISCO_LARGE; 1.
CC Photosynthesis; Carbon dioxide fixation; Photorespiration;
CC Lyase; Oxidoreductase; Monooxygenase; Chloroplast.
FT NON_TER 1 167
FT ACT_SITE 167 167 BINDING OF CO(2) ACTIVATES THE ENZYME
FT (BY SIMILARITY).
FT SEQUENCE 447 AA; 49663 MW; 6E56284E2C2DF270 CRC64;

Query Match

Best Local Similarity 76.2%; Score 32; DB 1; Length 447;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLRDDLLE 8
:|||||:

Db 314 LLRDDLVE 321

RESULT 12

RBL_PLAOC

ID RBL_PLAOC STANDARD; PRT; 465 AA.
AC P28441;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE RUBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO
DE LARGE SUBUNIT) (FRAGMENT).
DE RBL.
GN Platanus occidentalis (Sycamore).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Platanaceae; Platanus.
OX NCBL_TaxID=4403;
RN [1]
SEQUENCE FROM N.A.
RA MEDLINE=92397008; PubMed=1523408;
RA Albert V.A., Williams S.E., Chase M.W.;
RT "Carnivorous plants: phylogeny and structural evolution.";
RL Science 257:1491-1495(1992).
CC -!- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF
CC D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC
CC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF
CC THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
CC REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
CC ACTIVE SITE.
CC -!- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) =
CC 2 3-PHOSPHO-D-GLYCERATE.
CC -!- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) =
CC 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
CC -!- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- SIMILARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.
CC
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CC
CC EMBL; L01943; AAA84567.2; -
CC HSP; P00876; 3RUB.
CC InterPro: IPR000685; -
CC Pfam: PF00016; RUBISCO_large; 1.
CC PROSITE: PS00157; RUBISCO_LARGE; 1.
CC Photosynthesis; Carbon dioxide fixation; Photorespiration;
CC Lyase; Oxidoreductase; Monooxygenase; Chloroplast.
FT NON_TER 1 191
FT ACT_SITE 191 191 BINDING OF CO(2) ACTIVATES THE ENZYME.
FT SEQUENCE 465 AA; 51691 MW; E9DB5903CCF3BBAD CRC64;

Query Match

Best Local Similarity 76.2%; Score 32; DB 1; Length 465;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLRDDLLE 8
:|||||:

Db 338 LLRDDLVE 345

RESULT 13

RBL_TROAR

ID RBL_TROAR STANDARD; PRT; 465 AA.

AC P28458;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE RUBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO

DE LARGE SUBUNIT) (FRAGMENT).
GN RBCL.

OS Trochodendron aralioides.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; Trochodendraceae; Trochodendroideae;
 OC Trochodendron.
 OX NCBI_TaxID=4407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92397008; PubMed=1523408;
 RA Albert V.A., Williams S.E., Chase M.W.;
 RT "Carnivorous plants: phylogeny and structural evolution."; Science 257:1491-1495(1992).
 RL
 CC -----
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 CC -----
 CC EMBL: L01958; AA846595.2; ..
 CC HSSP: P00876; 3RUB.
 CC Mendel: 2879; TROAR:rbcl;1.
 CC InterPro: IPR000685; ..
 CC Pfam: PF00016; RUBISCO_large; 1.
 CC PROSITE: PS00157; RUBISCO_LARGE; 1.
 CC Photosynthesis; Carbon dioxide fixation; Photorespiration;
 KW Lyase; Oxidoreductase; Monooxygenase; Chloroplast.
 FT NON_TER 1 191
 FT ACT_SITE 1 191 BINDING OF CO(2) ACTIVATES THE ENZYME.
 FT SEQUENCE 465 AA; 51691 MW; E9DRS903CEP3B3AD CRC64;

Query Match 76.2%; Score 32; DB 1; Length 465;
 Best Local Similarity 75.0%; Pred. No. 51;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLRDOLLE 8
 DB 338 LLRDDLLE 345
 :|||||:

RESULT 14
 ID AMPA_CHLPN STANDARD; PRT; 499 AA.
 AC Q928F8; Q928F8;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PROBABLE CYTOSOL AMINOPEPTIDASE (EC 3.4.11.1) (LEUCINE AMINOPEPTIDASE)
 DE (LAP) (LEUCYL AMINOPEPTIDASE).
 GN PEPA OR CPN0385 OR CP0370.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CWL029;
 RX MEDLINE=99206606; PubMed=10192388;
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
 RL Nat. Genet. 21:385-389(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=AR39;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;

RT "genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 RL pneumoniae AR39."; Nucleic Acids Res. 28:1397-1406(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=J138;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RL from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
 CC -1- FUNCTION: PRESUMABLY INVOLVED IN THE PROCESSING AND REGULAR
 CC TURNOVER OF INTRACELLULAR PROTEINS. CATALYZES THE REMOVAL OF
 CC UNSUBSTITUTED AMINO-TERMINAL AMINO ACIDS FROM VARIOUS PEPTIDES (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: RELEASE OF AN N-TERMINAL AMINO ACID, XAA-[-
 CC XBB-], IN WHICH XAA IS PREFERABLY LEU, BUT MAY BE OTHER AMINO ACIDS
 CC INCLUDING PRO ALTHOUGH NOT ARG OR LYS, AND XBB MAY BE PRO.
 CC -1- COFACTOR: MANGANESE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M17; ALSO KNOWN AS THE
 CC CYTOSOL AMINOPEPTIDASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: AE001623; AAD18529.1; ..
 CC DR EMBL: AE002199; AAF38219.1; ..
 CC DR EMBL: AP002546; BAA98593.1; ..
 CC DR MEROPS; M17.003; ..
 CC DR TIGR: CP0370; ..
 CC DR HSSP: P00727; ILAN.
 CC DR InterPro: IPR000819; ..
 CC DR Pfam: PF00883; Peptidase_M17; 1.
 CC DR PRINTS: PR00481; LAMNOPPTDASE.
 CC DR PROSITE: PS00631; CYTOSOL_AP; 1.
 KW Hydrolase; Amino-peptidase; Manganese.
 FT METAL 263 263 MANGANESE (2) (BY SIMILARITY).
 FT METAL 268 268 MANGANESE (1 AND 2) (BY SIMILARITY).
 FT METAL 286 286 MANGANESE (2) (BY SIMILARITY).
 FT METAL 345 345 MANGANESE (1) (BY SIMILARITY).
 FT METAL 347 347 MANGANESE (1 AND 2) (BY SIMILARITY).
 FT ACT_SITE 275 275 POTENTIAL.
 FT ACT_SITE 349 349 POTENTIAL.
 FT SEQUENCE 499 AA; 54509 MW; B0F281B1DF4B9EC2 CRC64;

Query Match 76.2%; Score 32; DB 1; Length 499;
 Best Local Similarity 77.8%; Pred. No. 55;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLRDOLLE 9
 DB 395 VLAEDLLEA 403
 :|:|||||

RESULT 15
 ID CYSL_ECOLI STANDARD; PRT; 598 AA.
 AC P38038; P14782;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE SULFITE REDUCTASE [NADPH] FLAVOPROTEIN ALPHA-COMPONENT (EC 1.8.1.2)
 DE (SIR-FP).
 GN CYSL.
 OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_taxid=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-B;
 RX MEDLINE=89380164; PubMed=2550423;
 RA Ostrowski J., Barber M.J., Rueger D.C., Miller B.E., Siegel L.M.,
 RA Kredich N.M.;
 RT "Characterization of the flavoprotein moieties of NADPH-sulfite
 RT reductase from *Salmonella typhimurium* and *Escherichia coli*.
 RT Physicochemical and catalytic properties, amino acid sequence deduced
 RT from DNA sequence of *cysJ*, and comparison with NADPH-cytochrome P-450
 RT reductase.";
 RL J. Biol. Chem. 264:15796-15808(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE OF 593-598 FROM N.A.
 RC STRAIN-B;
 RX MEDLINE=89359425; PubMed=2670946;
 RA Ostrowski J., Wu J.-Y., Rueger D.C., Miller B.E., Siegel L.M.,
 RA Kredich N.M.;
 RT "Characterization of the *cysJH* regions of *Salmonella typhimurium* and
 RT *Escherichia coli* B. DNA sequences of *cysJ* and *cysH* and a model for
 RT the *siroheme-Fds4* active center of sulfite reductase hemoprotein
 RT based on amino acid homology with spinach nitrite reductase.";
 RL J. Biol. Chem. 264:15726-15737(1989).
 CC -!- FUNCTION: THIS ENZYME CATALYZES THE 6-ELECTRON REDUCTION OF
 CC SULFITE TO SULFIDE. THIS IS ONE OF SEVERAL ACTIVITIES REQUIRED
 CC FOR THE BIOSYNTHESIS OF L-CYSTEINE FROM SULFATE. THE FLAVO-
 CC PROTEIN COMPONENT CATALYZES THE ELECTRON FLOW FROM NADPH ->
 CC FAD -> FMN TO THE HEMOPROTEIN COMPONENT.
 CC -!- CATALYTIC ACTIVITY: HYDROGEN SULFIDE + 3 NADP(+) + 3 H(2)O =
 CC SULFITE + 3 NADPH.
 CC -!- COPACITOR: THIS SUBUNIT IS A FLAVOPROTEIN THAT BINDS ONE FMN AND
 CC ONE FAD PER CHAIN.
 CC -!- SUBUNIT: ALPHA(6)-BETA(4). THE ALPHA COMPONENT IS A FLAVOPROTEIN,
 CC THE BETA COMPONENT IS A HEMOPROTEIN.
 CC -----
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 CC -----
 DR EMBL; M23008; AAA23650.1; -;
 DR EMBL; U29579; AAA69274.1; -;
 DR EMBL; AE000360; AAC75806.1; -;
 DR PIR; B34231; B34231.
 DR HSSP; P00388; 1AMO.
 DR EcoGene; EG10191; *cysJ*.
 DR InterPro; IPR001094; -;
 DR InterPro; IPR001433; -;
 DR InterPro; IPR001709; -;
 DR InterPro; IPR003097; -;
 DR Pfam; PF00667; FAD_binding; 1.
 DR Pfam; PF00175; oxidored_fad; 1.
 DR PRINTS; PR00369; FLAVODOXIN.
 DR PRINTS; PR00371; FPNCR.
 KW Oxidoreductase; Flavoprotein; NADP; FAD; FMN; Electron transport;
 KW Cysteine biosynthesis.
 FT INIT_MET. 0

FT	NP_BIND	69	73	FMN (RIBITYLPHOSPHATE) (BY SIMILARITY).
FT	NP_BIND	149	180	FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT	NP_BIND	235	287	FAD (PYRROPHOSPHATE MOIETY) (BY SIMILARITY).
FT				(BY SIMILARITY).
FT	NP_BIND	471	598	NADP (PYRIMIDINE MOIETY) (BY SIMILARITY).
FT	CONFLICT	155	155	T -> S (IN REF. 2).
FT	CONFLICT	267	267	L -> M (IN REF. 2).
FT	CONFLICT	507	507	E -> D (IN REF. 2).
SQ	SEQUENCE	598 AA;	66148 MW;	OB6EEB0E2E70F13E CRC64;

Query Match 76.2%; Score 32; DB 1; Length 598;
 Best Local Similarity 87.5%; Pred No. 67;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LRDDLLAA 9
 | | | | | | |
 Db 81 LRDDLLAA 88

Search completed: July 10, 2001, 08:35:27
 Job time: 250 sec

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OM protein - protein search, using sw model

Run on: July 10, 2001, 08:32:06 ; Search time 18.74 Seconds
(without alignments)
9.675 Million cell updates/sec

Title: us-09-489-760-5
Perfect score: 42
Sequence: 1 VLRDLDLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues
Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	33	78.6	1045	1	US-08-452-083-2
2	31	73.8	251	5	PCT-US95-12357A-1
3	31	73.8	508	2	US-08-861-464-10
4	31	73.8	508	2	US-08-396-001-10
5	31	73.8	508	4	US-09-323-433A-10
6	31	73.8	593	3	US-08-556-419-22
7	31	73.8	629	3	US-08-556-419-23
8	31	73.8	2509	1	US-08-469-005A-10
9	30	71.4	483	2	US-08-770-544-8
10	30	71.4	821	1	US-07-935-311A-4
11	30	71.4	821	1	US-08-368-079-4
12	30	71.4	821	5	PCT-US93-07996-4
13	30	71.4	1159	2	US-08-956-242-13
14	30	71.4	1159	3	US-09-351-215-13
15	30	71.4	1159	4	US-09-226-012-2
16	30	71.4	1159	4	US-09-226-012-4
17	29	69.0	283	2	US-08-701-191A-41
18	29	69.0	790	1	US-08-363-560-2
19	29	69.0	1410	4	US-09-335-409-3
20	29	69.0	2165	1	US-08-514-975B-2
21	29	69.0	2165	5	PCT-US95-12507-2
22	29	69.0	2713	5	PCT-US96-01735-1
23	28	66.7	240	1	US-07-985-668A-3
24	28	66.7	240	2	US-08-950-433-3
25	28	66.7	240	3	US-09-186-287-3
26	28	66.7	245	4	US-08-944-483-69
27	28	66.7	275	2	US-09-016-366A-17

28 66.7 275 2 US-08-978-404B-12 Sequence 12, Appl
29 66.7 649 2 US-08-871-266B-16 Sequence 16, Appl
30 66.7 649 2 US-09-018-864A-16 Sequence 16, Appl
31 66.7 649 3 US-08-871-267B-22 Sequence 22, Appl
32 1832 4 US-09-335-409-4 Sequence 4, Appl
33 66.7 7257 4 US-09-335-409-5 Sequence 5, Appl
34 27 64.3 9 3 US-09-217-609A-11 Sequence 11, Appl
35 27 64.3 9 4 US-08-873-235B-11 Sequence 8, Appl
36 27 64.3 120 2 US-08-232-087A-8 Sequence 7, Appl
37 27 64.3 122 2 US-08-232-087A-7 Sequence 5, Appl
38 27 64.3 139 1 US-07-846-992-5 Sequence 5, Appl
39 27 64.3 139 1 US-08-469-555-5 Sequence 4, Appl
40 27 64.3 140 1 US-07-846-992-4 Sequence 6, Appl
41 27 64.3 140 1 US-08-469-555-4 Sequence 4, Appl
42 27 64.3 140 1 US-08-469-555-6 Sequence 6, Appl
43 27 64.3 140 1 US-07-855-412B-1 Sequence 1, Appl
44 27 64.3 200 1 US-07-855-412B-1 Sequence 1, Appl
45 27 64.3 200 2 US-08-308-887A-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-452-083-2
; Sequence 2, Application US/08452083
; Patent No. 5756327
; GENERAL INFORMATION:
; APPLICANT: Sassanfar, Mandana
; APPLICANT: Schimmel, Paul R.
; TITLE OF INVENTION: RECOMBINANT MYCOBACTERIAL ISOLEUCYL-L-LENA
; TITLE OF INVENTION: SYNTHETASE GENES, TESTER STRAINS AND ASSAYS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452.083
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/305,765
; FILING DATE: 13-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CPI94-08B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1045 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-452-083-2

Query Match 78.6%; Score 33; DB 1; Length 1045;
Best Local Similarity 77.8%; Pred. No. 82;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLRDLDLEA 9

Db 720 VLRLDLS 728
 ||||| |

RESULT 2

US-08-861-464-10
 : Sequence 10, Application US/08861464
 : Patent No. 5874210
 : GENERAL INFORMATION:
 : APPLICANT: Guarente, Leonard P.
 : APPLICANT: Austriaco Jr., Nicanor
 : APPLICANT: Kennedy, Brian
 : TITLE OF INVENTION: Genes Determining Cellular Senescence in Yeast
 : NUMBER OF SEQUENCES: 13
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
 : STREET: 1100 New York Avenue, N.W.
 : CITY: Washington
 : STATE: DC
 : COUNTRY: USA
 : ZIP: 20005
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC Compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION NUMBER: PCT/US95/12357A
 : FILING DATE: 29-SEPT-1995
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/316,419
 : FILING DATE: 30-SEPT-1994
 : CLASSIFICATION:
 : APPLICATION NUMBER: 08/471,100
 : FILING DATE: 6-JUNE-1995
 : CLASSIFICATION:
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Fox, Samuel L.
 : REGISTRATION NUMBER: 30,353
 : REFERENCE/DOCKET NUMBER: 0656.048PC01
 : TELEPHONE: 202-371-2600
 : TELEFAX: 202-371-2540
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 251 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: not relevant
 : TOPOLOGY: not relevant
 : MOLECULE TYPE: peptide
 : PCT-US95-12357A-1

Query Match 73.8%; Score 31; DB 5; Length 251;
 Best Local Similarity 85.7%; Pred No. 42;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLLE 8

Db 228 LKDDLLE 234

RESULT 3

US-08-861-464-10
 : Sequence 10, Application US/08861464
 : Patent No. 5874210
 : GENERAL INFORMATION:
 : APPLICANT: Guarente, Leonard P.
 : APPLICANT: Austriaco Jr., Nicanor
 : APPLICANT: Kennedy, Brian
 : TITLE OF INVENTION: Genes Determining Cellular Senescence in Yeast
 : NUMBER OF SEQUENCES: 16
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 : STREET: Two Militia Drive
 : CITY: Lexington
 : STATE: MA
 : COUNTRY: USA
 : ZIP: 02173
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk

US-08-396-001-10
 : Sequence 10, Application US/08396001
 : Patent No. 5919618
 : GENERAL INFORMATION:
 : APPLICANT: Guarente, Leonard P.
 : APPLICANT: Austriaco Jr., Nicanor
 : APPLICANT: Claus, James
 : APPLICANT: Cole, Francesca
 : APPLICANT: Kennedy, Brian
 : TITLE OF INVENTION: Genes Determining Cellular Senescence in Yeast
 : NUMBER OF SEQUENCES: 16
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 : STREET: Two Militia Drive
 : CITY: Lexington
 : STATE: MA
 : COUNTRY: USA
 : ZIP: 02173
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC Compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION NUMBER: US/08/861,464
 : FILING DATE: 22-MAY-1997
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/396,001
 : FILING DATE: 28-FEB-1995
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: PCT/US94/09351
 : FILING DATE: 15-AUG-1994
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/107,408
 : FILING DATE: 16-AUG-1993
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Granahan, Patricia
 : REGISTRATION NUMBER: 32,227
 : REFERENCE/DOCKET NUMBER: MIT-6408A22
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 781-861-6240
 : TELEFAX: 781-861-9540
 : INFORMATION FOR SEQ ID NO: 10:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 508 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-861-464-10

Query Match 73.8%; Score 31; DB 2; Length 508;
 Best Local Similarity 85.7%; Pred. No. 93;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLLE 8

Db 62 LRDDLVE 68

RESULT 4

US-08-396-001-10
 : Sequence 10, Application US/08396001
 : Patent No. 5919618
 : GENERAL INFORMATION:
 : APPLICANT: Guarente, Leonard P.
 : APPLICANT: Austriaco Jr., Nicanor
 : APPLICANT: Claus, James
 : APPLICANT: Cole, Francesca
 : APPLICANT: Kennedy, Brian
 : TITLE OF INVENTION: Genes Determining Cellular Senescence in Yeast
 : NUMBER OF SEQUENCES: 16
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 : STREET: Two Militia Drive
 : CITY: Lexington
 : STATE: MA
 : COUNTRY: USA
 : ZIP: 02173
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: Ross, Christopher
FILING DATE: 28-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MT-6408A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-9540
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 508 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-396-001-10

Query Match 73.8%; Score 31; DB 2; Length 508;
Best Local Similarity 85.7%; Pred. No. 93;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLLE 8
Db 62 LRDDLVE 68
|||||:1

RESULT 5
US-09-323-433A-10
Sequence 10, Application US/09323433A
Patent No. 6218512
GENERAL INFORMATION:
APPLICANT: Guarente, Leonard P.
APPLICANT: Austriaco Jr., Nicanor
APPLICANT: Claus, James J.
APPLICANT: Cole, Francesca
APPLICANT: Kennedy, Brian
TITLE OF INVENTION: GENES DETERMINING CELLULAR SENESCENCE IN YEAST
FILE REFERENCE: 0050.1491-003
CURRENT APPLICATION NUMBER: US/09/323,433A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: US 08/396,001
PRIOR FILING DATE: 1995-02-28
PRIOR APPLICATION NUMBER: PCT/US94/09351
PRIOR FILING DATE: 1994-08-15
PRIOR APPLICATION NUMBER: US 08/107,408
PRIOR FILING DATE: 1993-08-16
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 508
TYPE: PRT
ORGANISM: Homo sapiens
US-09-323-433A-10

Query Match 73.8%; Score 31; DB 4; Length 508;
Best Local Similarity 85.7%; Pred. No. 93;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLLE 8
Db 62 LRDDLVE 68
|||||:1

RESULT 6
US-08-556-419-22

Sequence 22, Application US/08556419C
Patent No. 6093549
GENERAL INFORMATION:
APPLICANT: Ross, Christopher
APPLICANT: Li, Xiao-Jiang
APPLICANT: Li, Shi-Hua
APPLICANT: Sharp, Alan
APPLICANT: Lanahan, Anthony
APPLICANT: Worley, Paul
APPLICANT: Snyder, Solomon
TITLE OF INVENTION: Huntingtin-associated protein
FILE REFERENCE: 01107.52271
CURRENT APPLICATION NUMBER: US/08/556,419C
CURRENT FILING DATE: 1995-11-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 22
LENGTH: 599
TYPE: PRT
ORGANISM: Rattus norvegicus
US-08-556-419-22

Query Match 73.8%; Score 31; DB 3; Length 599;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLLE 8
Db 205 LRDDLQ 211
|||||:

RESULT 7
US-08-556-419-23
Sequence 23, Application US/08556419C
Patent No. 6093549
GENERAL INFORMATION:
APPLICANT: Ross, Christopher
APPLICANT: Li, Xiao-Jiang
APPLICANT: Li, Shi-Hua
APPLICANT: Sharp, Alan
APPLICANT: Lanahan, Anthony
APPLICANT: Worley, Paul
APPLICANT: Snyder, Solomon
TITLE OF INVENTION: Huntingtin-associated protein
FILE REFERENCE: 01107.52271
CURRENT APPLICATION NUMBER: US/08/556,419C
CURRENT FILING DATE: 1995-11-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 23
LENGTH: 629
TYPE: PRT
ORGANISM: Rattus norvegicus
US-08-556-419-23

Query Match 73.8%; Score 31; DB 3; Length 629;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLLE 8
Db 205 LRDDLQ 211
|||||:

RESULT 8
US-08-469-005A-10
Sequence 10, Application US/08469005A
Patent No. 5665874
GENERAL INFORMATION:
APPLICANT: KUHAJDA, FRANCIS P.
APPLICANT: PASTERNAK, GARY A.

```

; TITLE OF INVENTION: CANCER RELATED ANTIGEN
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,005A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/188,426
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 08/096,908
; FILING DATE: 26-JUL-1993
; APPLICATION NUMBER: 07/917,716
; FILING DATE: 24-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: POSORSKE, Laurence H
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 062482-0113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-639-7700
; TELEFAX: 202-639-7890
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2509 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-469-005A-10

Query Match 73.8%; Score 31; DB 1; Length 2509;
Best Local Similarity 87.5%; Pred. No. 5.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLRRDLLE 8
DB 1972 VLRRDLLE 1979

RESULT 9
US-08-770-544-8
; Sequence 8, Application US/08770544
; Patent No. 5907085
; GENERAL INFORMATION:
; APPLICANT: Gonsalves, Dennis
; APPLICANT: Ling, Kai-Shu
; TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND
; TITLE OF INVENTION: THEIR USES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603

```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,544
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60009008
; FILING DATE: 21-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/621
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 483 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-770-544-8

Query Match 71.4%; Score 30; DB 2; Length 483;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RDDLEA 9
DB 124 RDDLEA 130

RESULT 10
US-07-935-311A-4
; Sequence 4, Application US/07935311A
; Patent No. 5378809
; GENERAL INFORMATION:
; APPLICANT: Di Fiore, Pier Paolo
; APPLICANT: Fazioli, Francesca
; TITLE OF INVENTION: Substrate of the Epidermal Growth
; TITLE OF INVENTION: Factor Kinase
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92560
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,311A
; FILING DATE: 19920825
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelson, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH035.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

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LENGTH: 821 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-935-311A-4

Query Match 71.4%; Score 30; DB 1; Length 821;
Best Local Similarity 62.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLRDLDLLE 8
|::|::|::|
Db 551 VMKDDVLE 558

RESULT 11

US-08-368-079-4
Sequence 4, Application US/08368079

Patent No. 5610018

GENERAL INFORMATION:

APPLICANT: Di Fiore, Pier Paolo

APPLICANT: Fazioli, Francesca

TITLE OF INVENTION: eps8, A Substrate for the Epidermal Growth Factor

TITLE OF INVENTION: Kinase, Antibodies Thereto, and Methods of Use Thereof

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear

STREET: 620 Newport Center Drive, 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: USA

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/368,079

FILING DATE: 03-JAN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/935,311

FILING DATE: 25-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: Israelsen, Ned A.

REGISTRATION NUMBER: 29,655

REFERENCE/DOCKET NUMBER: NIH035.001DV1

TELEPHONE: (619) 235-8550

TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 821 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-368-079-4

Query Match 71.4%; Score 30; DB 1; Length 821;
Best Local Similarity 62.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLRDLDLLE 8
|::|::|::|
Db 551 VMKDDVLE 558

RESULT 12

PCT-US93-07996-4

Sequence 4, Application PC/TUS9307996

GENERAL INFORMATION:

APPLICANT: The Government of the United States, as represented by the

APPLICANT: Secretary of Health and Human Services

TITLE OF INVENTION: Substrate of the Epidermal Growth Factor Kinase

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear

STREET: 620 Newport Center Drive, 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: USA

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/07996

FILING DATE: 19930825

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550

TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 821 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US93-07996-4

Query Match 71.4%; Score 30; DB 5; Length 821;
Best Local Similarity 62.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLRDLDLLE 8
|::|::|::|
Db 551 VMKDDVLE 558

RESULT 13

US-08-956-242-13

Sequence 13, Application US/08956242C

Patent No. 5986081

GENERAL INFORMATION:

APPLICANT: Ganetzky, Barry S.

APPLICANT: Titus, Steven A.

TITLE OF INVENTION: Polynucleotides Encoding Herg-3

FILE REFERENCE: 960296.94550

CURRENT APPLICATION NUMBER: US/08/956,242C

CURRENT FILING DATE: 1997-10-22

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patent Ver. 2.0

SEQ ID NO 13

LENGTH: 1159

TYPE: PRT

ORGANISM: Homo sapien

US-08-956-242-13

Query Match 71.4%; Score 30; DB 2; Length 1159;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RDDLLE 8
|::|::|::|
Db 835 RDDLLE 840

RESULT 14

US-09-351-215-13

Sequence 13, Application US/09351215

; Patent No. 6087488
; GENERAL INFORMATION:
; APPLICANT: Ganetzky, Barry S.
; TITLE OF INVENTION: Polynucleotides Encoding Herg-3
; FILE REFERENCE: 960296.94550
; CURRENT APPLICATION NUMBER: US/09/351.215
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 08/956.242
; EARLIER FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 1159
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-351-215-13

Query Match 71.4%; Score 30; DB 3; Length 1159;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RDDLLE 8
Db 835 RDDLLE 840

RESULT 15
US-09-226-012-2
; Sequence 2, Application US/09226012
; Patent No. 6207383
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
; FILE REFERENCE: 2323-136
; CURRENT APPLICATION NUMBER: US/09/226.012
; CURRENT FILING DATE: 1999-01-06
; EARLIER APPLICATION NUMBER: 09/122.847
; EARLIER FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1159
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-226-012-2

Query Match 71.4%; Score 30; DB 4; Length 1159;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RDDLLE 8
Db 835 RDDLLE 840

Search completed: July 10, 2001, 08:32:07
Job time: 150 sec

Tue Jul 10 13:30:21 2001

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 10, 2001, 08:36:07 ; Search time 33.27 Seconds
(without alignments)
35.790 Million cell up

Title: US-09-489-760-5
Perfect score: 42
Sequence: 1 VLRDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues
Total number of hits satisfying chosen parameters: 425026

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

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Database :
SPREMBL_16:*
1:  sp.archaea:*
2:  sp.bacteria:*
3:  sp.fungi:*
4:  sp.human:*
5:  sp.invertebrate:*
6:  sp.mammal:*
7:  sp.mhc:*
8:  sp.organelle:*
9:  sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.unclassified:*
13: sp.vertebrate:*
14: sp.virus:*
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SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	42	100.0	1765	4	Q92619	Q92619 homo sapien
2	38	90.5	1650	4	Q9K1V4	Q9K1V4 streptomyce
3	36	85.7	174	5	Q94256	Q94256 caenorhabd.
4	35	83.3	616	1	O37025	O27025 methanobact.
5	34	81.0	238	14	Q9WHX7	Q9WHX7 influenza a
6	34	81.0	239	14	Q9WHY9	Q9WHY9 influenza a
7	34	81.0	239	14	Q9WHY8	Q9WHY8 influenza a
8	34	81.0	239	14	Q9WHY7	Q9WHY7 influenza a
9	34	81.0	239	14	Q9WHY6	Q9WHY6 influenza a
10	34	81.0	239	14	Q9WHY5	Q9WHY5 influenza a
11	34	81.0	239	14	Q9WHY4	Q9WHY4 influenza a
12	34	81.0	239	14	Q9WHY3	Q9WHY3 influenza a
13	34	81.0	239	14	Q9WHY1	Q9WHY1 influenza a
14	34	81.0	239	14	Q9WHX9	Q9WHX9 influenza a
15	34	81.0	250	14	Q9WHY2	Q9WHY2 influenza a
16	34	81.0	252	14	Q93188	Q93188 influenza a
17	34	81.0	389	5	Q9XRD7	Q9XRD7 caenorhabd
18	34	81.0	486	2	Q9PPU0	Q9PPU0 ureaplasma
19	34	81.0	791	5	Q9NG78	Q9NG78 caenorhabd

ALIGNMENTS

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RESULT      1
092619     PRELIMINARY;          PRT;   1165 AA.
ACID       Q92619;
AC         Q92619;
DT         01-FEB-1997 (TrEMBLrel. 02, Created)
DT         01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT         01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE         MYELOBLAST KIAA0223 (FRAGMENT).
EN         KIAA0223.
OS         Homo sapiens (Human).
OC         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX         NCBI_TaxId=9606;
[1]
SEQUENCE FROM N.A.
TSSU     TISSUE=BONE MARROW;
MEDLIN    MEDLINE=97191544; PubMed=9039502;
NAGASE    Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayashi Y., Ohara O.,
TANAKA    Tanaka A., Kotani H., Miyajima N., Nomura N.;
PRT       "Prediction of the coding sequences of unidentified human genes. VI.
PRT       The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
PRT       analysis of cDNA clones from cell line KG-1 and brain.";
PRT       DNA Res. 3:321-329(1996).
[2]
SEQUENCE OF 170-1165 FROM N.A.
LAMERDIN  Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
BURKHARDT Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
PHAN H., Velasco N., Ganes J., Danganan L., Poundstone P.,
CHRISTENSE Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T.,
TRUCKHEIM Truckheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,
BRUCE R., Thomas P., Quan G., Kronmiller B., Arellano A.,
MONTGOMERY Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,
CARRANO    Carrano A.V.;
SUBMITTED (FEB-1998) to the ENBL/GenBank/DBJ databasés.
EMBL; D86976; BAA13212.1; --
EMBL; AC004151; AAC03237.1; --
HSSP; Q07960; IJGF.
InterPro; IPR000198; --
InterPro; IPR002219; --
Pfam; PF001130; DAG_PP-bind; 1.
Pfam; PF006020; RhOGAP; 1.
PROSITE; PS00479; DAG_PP_BIND_DOM_1; UNKNOWN_1.

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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 Rhabditidae; Peloderinae; Caenorhabditis.
 NCBI_TaxID=6239;
 [1]
 SEQUENCE FROM N.A.
 STRAIN-BRISTOL N2;
 MEDLINE=94150718; PubMed=7906398;
 Willson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 Granger A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 Lightning J., Lloyd J.C., McMurray A., Montmore B., O'Callaghan M.,
 Parsons J., Percy C., Rifken L., Roopya A., Saunders D., Showkeen R.,
 Smauldin K., Smith A., Sonhammer E., Staden K., Sulston J.,
 Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 Watson A., Weinstein L., Wilkins-Sproat J., Wohlman P.;
 "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C.
 elegans*.";
 Nature 368:32-38(1994).
 [2]
 SEQUENCE FROM N.A.
 STRAIN-BRISTOL N2;
 Gelsel C., Bradshaw H.;
 Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 EMBL; U64849; AAC49055.1; -;
 InterPro; IPR000004; -;
 SMART; SM00118; SAPB; 1.
 SEQUENCE 174 AA; 19210 MW; A6303CF6383BEBD9 CRC64;

 Query Match 85.7%; Score 36; DB 5; Length 174;
 Best Local Similarity 77.8%; Pred. No. 23;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

 QY 1 VLRODLLEA 9
 ||:||||:|
 DB 129 VLKODLLDA 137

 RESULT 4
 Q27025 PRELIMINARY; PRT; 616 AA.
 ID O27025
 AC O27025;
 DT 01-JAN-1998 (TRENBLREL 05, Created)
 DT 01-JAN-1998 (TRENBLREL 05, Last-sequence update)
 DT 01-MAR-2001 (TRENBLREL 16, Last annotation update)
 DE TYPE I RESTRICTION MODIFICATION ENZYME, SUBUNIT M.
 MT942.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
 OC Methanothermobacter.
 OX NCBI_TaxID=145262;
 OX NCBI
 [1]
 SEQUENCE FROM N.A.
 STRAIN-DELTA H;
 MEDLINE=98037514; PubMed=93711463;
 Smith D.R., Ducette-Stamm L.A., Deloughery C., Lee H.-M., DuBois J.,
 Aldredge T., Bashirzaden R., Blakely D., Cook R., Gilbert K.,
 Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
 Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 Jiwni N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
 Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
 "Complete genome sequence of *Methanobacterium thermoautotrophicum*
 deltaH: functional analysis and comparative genomics.";
 J. Bacteriol. 179:7135-7155(1997).
 EMBL; AE000868; AB85440.1; -;
 InterPro; IPR002052; -;
 InterPro; IPR002296; -;
 InterPro; IPR003356; -;
 Pfam; PF02384; N6_Mtase; 1.
 PRINTS; PR00507; N12N6MTFRASE.

